

(1) GENERAL INFORMATION:

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(iii) NUMBER OF SEQUENCES: 47

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1277 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

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(A) NAME/KEY: CDS
(B) LOCATION: 1..1275

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

15	ATG GTC GAA ATG CTG CTG TTG ACA AGA ATT CTC TTG GTG GGC TTC ATC	48
	Met Val Glu Met Leu Leu Leu Thr Arg Ile Leu Leu Val Gly Phe Ile	
	1 5 10 15	
20	TGC GCT CTT TTA GTC TCC TCT GGG CTG ACT TGT GGA CCA GGC AGG GGC	96
	Cys Ala Leu Leu Val Ser Ser Gly Leu Thr Cys Gly Pro Gly Arg Gly	
	20 25 30	
25	ATT GGA AAA AGG AGG CAC CCC AAA AAG CTG ACC CCG TTA GCC TAT AAG	144
	Ile Gly Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys	
	35 40 45	
30	CAG TTT ATT CCC AAT GTG GCA GAG AAG ACC CTA GGG GCC AGT GGA AGA	192
	Gln Phe Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg	
	50 55 60	
35	TAT GAA GGG AAG ATC ACA AGA AAC TCC GAG AGA TTT AAA GAA CTA ACC	240
	Tyr Glu Gly Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr	
	65 70 75 80	
40	CCA AAT TAC AAC CCT GAC ATT ATT TTT AAG GAT GAA GAG AAC ACG GGA	288
	Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly	
	85 90 95	
45	GCT GAC AGA CTG ATG ACT CAG CGC TGC AAG GAC AAG CTG AAT GCC CTG	336
	Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ala Leu	
	100 105 110	
50	GCG ATC TCG GTG ATG AAC CAG TGG CCC GGG GTG AAG CTG CGG GTG ACC	384
	Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg Val Thr	
	115 120 125	
55	GAG GGC TGG GAC GAG GAT GGC CAT CAC TCC GAG GAA TCG CTG CAC TAC	432
	Glu Gly Trp Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr	
	130 135 140	
60	GAG GGT CGC GCC GTG GAC ATC ACC ACG TCG GAT CGG GAC CGC AGC AAG	480
	Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg Ser Lys	
	145 150 155 160	
65	TAC GGA ATG CTG GCC CGC CTC GCC GTC GAG GCC GGC TTC GAC TGG GTC	528
	Tyr Gly Met Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val	
	165 170 175	

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	TAC TAC GAG TCC AAG GCG CAC ATC CAC TGC TCC GTC AAA GCA GAA AAC	576
	Tyr Tyr Glu Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn	
	180 185 190	
5	TCA GTG GCA GCG AAA TCA GGA GGC TGC TTC CCT GGC TCA GCC ACA GTG	624
	Ser Val Ala Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Thr Val	
	195 200 205	
10	CAC CTG GAG CAT GGA GGC ACC AAG CTG GTG AAG GAC CTG AGC CCT GGG	672
	His Leu Glu His Gly Gly Thr Lys Leu Val Lys Asp Leu Ser Pro Gly	
	210 215 220	
15	GAC CGC GTG CTG GCT GCT GAC GCG GAC GGC CGG CTG CTC TAC AGT GAC	720
	Asp Arg Val Leu Ala Ala Asp Ala Asp Gly Arg Leu Leu Tyr Ser Asp	
	225 230 235 240	
20	TTC CTC ACC TTC CTC GAC CGG ATG GAC AGC TCC CGA AAG CTC TTC TAC	768
	Phe Leu Thr Phe Leu Asp Arg Met Asp Ser Ser Arg Lys Leu Phe Tyr	
	245 250 255	
25	GTC ATC GAG ACG CGG CAG CCC CGG GCC CGG CTG CTA CTG ACG GCG GCC	816
	Val Ile Glu Thr Arg Gln Pro Arg Ala Arg Leu Leu Leu Thr Ala Ala	
	260 265 270	
30	CAC CTG CTC TTT GTG GCC CCC CAG CAC AAC CAG TCG GAG GCC ACA GGG	864
	His Leu Leu Phe Val Ala Pro Gln His Asn Gln Ser Glu Ala Thr Gly	
	275 280 285	
35	TCC ACC AGT GGC CAG GCG CTC TTC GCC AGC AAC GTG AAG CCT GGC CAA	912
	Ser Thr Ser Gly Gln Ala Leu Phe Ala Ser Asn Val Lys Pro Gly Gln	
	290 295 300	
40	CGT GTC TAT GTG CTG GGC GAG GGC GGG CAG CAG CTG CTG CCG GCG TCT	960
	Arg Val Tyr Val Leu Gly Glu Gly Gly Gln Gln Leu Leu Pro Ala Ser	
	305 310 315 320	
45	GTC CAC AGC GTC TCA TTG CGG GAG GAG GCG TCC GGA GCC TAC GCC CCA	1008
	Val His Ser Val Ser Leu Arg Glu Glu Ala Ser Gly Ala Tyr Ala Pro	
	325 330 335	
50	CTC ACC GCC CAG GGC ACC ATC CTC ATC AAC CGG GTG TTG GCC TCC TGC	1056
	Leu Thr Ala Gln Gly Thr Ile Leu Ile Asn Arg Val Leu Ala Ser Cys	
	340 345 350	
55	TAC GCC GTC ATC GAG GAG CAC AGT TGG GCC CAT TGG GCC TTC GCA CCA	1104
	Tyr Ala Val Ile Glu Glu His Ser Trp Ala His Trp Ala Phe Ala Pro	
	355 360 365	
60	TTC CGC TTG GCT CAG GGG CTG CTG GCC GCC CTC TGC CCA GAT GGG GCC	1152
	Phe Arg Leu Ala Gln Gly Leu Leu Ala Ala Leu Cys Pro Asp Gly Ala	
	370 375 380	
65	ATC CCT ACT GCC GCC ACC ACC ACC ACT GGC ATC CAT TGG TAC TCA CGG	1200
	Ile Pro Thr Ala Ala Thr Thr Thr Thr Gly Ile His Trp Tyr Ser Arg	
	385 390 395 400	
70	CTC CTC TAC CGC ATC GGC AGC TGG GTG CTG GAT GGT GAC GCG CTG CAT	1248
	Leu Leu Tyr Arg Ile Gly Ser Trp Val Leu Asp Gly Asp Ala Leu His	

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405 410 415 1277

CCG CTG GGC ATG GTG GCA CCG GCC AGC TG
 Pro Leu Gly Met Val Ala Pro Ala Ser

5 420 425

(2) INFORMATION FOR SEQ ID NO:2:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1190 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: cDNA

20 (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..1191

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATG GCT CTG CCG GCC AGT CTG TTG CCC CTG TGC TGC TTG GCA CTC TTG 48
 Met Ala Leu Pro Ala Ser Leu Leu Pro Leu Cys Cys Leu Ala Leu Leu
 1 5 10 15

GCA CTA TCT GCC CAG AGC TGC GGG CCG GGC CGA GGA CCG GTT GGC CGG 96
 Ala Leu Ser Ala Gln Ser Cys Gly Pro Gly Arg Gly Pro Val Gly Arg
 20 25 30

CGG CGT TAT GTG CGC AAG CAA CTT GTG CCT CTG CTA TAC AAG CAG TTT 144
 Arg Arg Tyr Val Arg Lys Gln Leu Val Pro Leu Leu Tyr Lys Gln Phe
 35 40 45

GTG CCC AGT ATG CCC GAG CGG ACC CTG GGC GCG AGT GGG CCA GCG GAG 192
 Val Pro Ser Met Pro Glu Arg Thr Leu Gly Ala Ser Gly Pro Ala Glu
 50 55 60

GGG AGG GTA ACA AGG GGG TCG GAG CGC TTC CGG GAC CTC GTA CCC AAC 240
 Gly Arg Val Thr Arg Gly Ser Glu Arg Phe Arg Asp Leu Val Pro Asn
 45 65 70 75 80

TAC AAC CCC GAC ATA ATC TTC AAG GAT GAG GAG AAC AGC GGC GCA GAC 288
 Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Ser Gly Ala Asp
 85 90 95

CGC CTG ATG ACA GAG CGT TGC AAA GAG CGG GTG AAC GCT CTA GCC ATC 336
 Arg Leu Met Thr Glu Arg Cys Lys Glu Arg Val Asn Ala Leu Ala Ile
 100 105 110

GCG GTG ATG AAC ATG TGG CCC GGA GTA CGC CTA CGT GTG ACT GAA GGC 384
 Ala Val Met Asn Met Trp Pro Gly Val Arg Leu Arg Val Thr Glu Gly
 115 120 125

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	Trp	Asp	Glu	Asp	Gly	His	His	Ala	Gln	Asp	Ser	Leu	His	Tyr	Glu	Gly	432
	130						135						140				
5	CGT	GCC	TTG	GAC	ATC	ACC	ACG	TCT	GAC	CGT	GAC	CGT	AAT	AAG	TAT	GGT	480
	Arg	Ala	Leu	Asp	Ile	Thr	Thr	Ser	Asp	Arg	Asp	Arg	Asn	Lys	Tyr	Gly	
	145					150					155					160	
10	TTG	TTG	GCG	CGC	CTA	GCT	GTG	GAA	GCC	GGA	TTC	GAC	TGG	GTC	TAC	TAC	528
	Leu	Leu	Ala	Arg	Leu	Ala	Val	Glu	Ala	Gly	Phe	Asp	Trp	Val	Tyr	Tyr	
					165					170						175	
15	GAG	TCC	CGC	AAC	CAC	ATC	CAC	GTA	TCG	GTC	AAA	GCT	GAT	AAC	TCA	CTG	576
	Glu	Ser	Arg	Asn	His	Ile	His	Val	Ser	Val	Lys	Ala	Asp	Asn	Ser	Leu	
				180					185					190			
20	GCG	GTC	CGA	GCC	GGA	GGC	TGC	TTT	CCG	GGA	AAT	GCC	ACG	GTG	CGC	TTG	624
	Ala	Val	Arg	Ala	Gly	Gly	Cys	Phe	Pro	Gly	Asn	Ala	Thr	Val	Arg	Leu	
			195					200					205				
25	CGG	AGC	GGC	GAA	CGG	AAG	GGG	CTG	AGG	GAA	CTA	CAT	CGT	GGT	GAC	TGG	672
	Arg	Ser	Gly	Glu	Arg	Lys	Gly	Leu	Arg	Glu	Leu	His	Arg	Gly	Asp	Trp	
		210					215					220					
30	GTA	CTG	GCC	GCT	GAT	GCA	GCG	GGC	CGA	GTG	GTA	CCC	ACG	CCA	GTG	CTG	720
	Val	Leu	Ala	Ala	Asp	Ala	Ala	Gly	Arg	Val	Val	Pro	Thr	Pro	Val	Leu	
	225					230					235					240	
35	CTC	TTC	CTG	GAC	CGG	GAT	CTG	CAG	CGC	CGC	GCC	TCG	TTC	GTG	GCT	GTG	768
	Leu	Phe	Leu	Asp	Arg	Asp	Leu	Gln	Arg	Arg	Ala	Ser	Phe	Val	Ala	Val	
					245					250					255		
40	GAG	ACC	GAG	CGG	CCT	CCG	CGC	AAA	CTG	TTG	CTC	ACA	CCC	TGG	CAT	CTG	816
	Glu	Thr	Glu	Arg	Pro	Pro	Arg	Lys	Leu	Leu	Leu	Thr	Pro	Trp	His	Leu	
				260				265						270			
45	GTG	TTC	GCT	GCT	CGC	GGG	CCA	GCG	CCT	GCT	CCA	GGT	GAC	TTT	GCA	CCG	864
	Val	Phe	Ala	Ala	Arg	Gly	Pro	Ala	Pro	Ala	Pro	Gly	Asp	Phe	Ala	Pro	
			275					280					285				
50	GTG	TTC	GCG	CGC	CGC	TTA	CGT	GCT	GGC	GAC	TCG	GTG	CTG	GCT	CCC	GGC	912
	Val	Phe	Ala	Arg	Arg	Leu	Arg	Ala	Gly	Asp	Ser	Val	Leu	Ala	Pro	Gly	
		290					295					300					
55	GGG	GAC	GCG	CTC	CAG	CCG	GCG	CGC	GTA	GCC	CGC	GTG	GCG	CGC	GAG	GAA	960
	Gly	Asp	Ala	Leu	Gln	Pro	Ala	Arg	Val	Ala	Arg	Val	Ala	Arg	Glu	Glu	
	305					310					315					320	
60	GCC	GTG	GGC	GTG	TTC	GCA	CCG	CTC	ACT	GCG	CAC	GGG	ACG	CTG	CTG	GTC	1008
	Ala	Val	Gly	Val	Phe	Ala	Pro	Leu	Thr	Ala	His	Gly	Thr	Leu	Leu	Val</	

	355	360	365	
	CTG CTC CCT GGG GGT GCA GTC CAG CCG ACT GGC ATG CAT TGG TAC TCT			1152
5	Leu Leu Pro Gly Gly Ala Val Gln Pro Thr Gly Met His Trp Tyr Ser			
	370	375	380	
	CGC CTC CTT TAC CGC TTG GCC GAG GAG TTA ATG GGC TG			1190
	Arg Leu Leu Tyr Arg Leu Ala Glu Glu Leu Met Gly			
10	385	390	395	
(2) INFORMATION FOR SEQ ID NO:3:				
	(i) SEQUENCE CHARACTERISTICS:			
15	(A) LENGTH: 1281 base pairs			
	(B) TYPE: nucleic acid			
	(C) STRANDEDNESS: both			
	(D) TOPOLOGY: linear			
20	(ii) MOLECULE TYPE: cDNA			
	(ix) FEATURE:			
25	(A) NAME/KEY: CDS			
	(B) LOCATION: 1..1233			
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:			
30	ATG TCT CCC GCC TGG CTC CGG CCC CGA CTG CGG TTC TGT CTG TTC CTG			48
	Met Ser Pro Ala Trp Leu Arg Pro Arg Leu Arg Phe Cys Leu Phe Leu			
	1	5	10	15
35	CTG CTG CTG CTT CTG GTG CCG GCG GCG CGG GGC TGC GGG CCG GGC CGG			96
	Leu Leu Leu Leu Leu Val Pro Ala Ala Arg Gly Cys Gly Pro Gly Arg			
	20	25	30	
40	GTG GTG GGC AGC CGC CGG AGG CCG CCT CGC AAG CTC GTG CCT CTT GCC			144
	Val Val Gly Ser Arg Arg Arg Pro Pro Arg Lys Leu Val Pro Leu Ala			
	35	40	45	
45	TAC AAG CAG TTC AGC CCC AAC GTG CCG GAG AAG ACC CTG GGC GCC AGC			192
	Tyr Lys Gln Phe Ser Pro Asn Val Pro Glu Lys Thr Leu Gly Ala Ser			
	50	55	60	
50	GGG CGC TAC GAA GGC AAG ATC GCG CGC AGC TCT GAG CGC TTC AAA GAG			240
	Gly Arg Tyr Glu Gly Lys Ile Ala Arg Ser Ser Glu Arg Phe Lys Glu			
	65	70	75	80
55	CTC ACC CCC AAC TAC AAT CCC GAC ATC ATC TTC AAG GAC GAG GAG AAC			288
	Leu Thr Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn			
	85	90	95	
55	ACG GGT GCC GAC CGC CTC ATG ACC CAG CGC TGC AAG GAC CGT CTG AAC			336
	Thr Gly Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Arg Leu Asn			
	100	105	110	

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	TCA	CTG	GCC	ATC	TCT	GTC	ATG	AAC	CAG	TGG	CCT	GGT	GTG	AAA	CTG	CGG	384
	Ser	Leu	Ala	Ile	Ser	Val	Met	Asn	Gln	Trp	Pro	Gly	Val	Lys	Leu	Arg	
			115					120					125				
5	GTG	ACC	GAA	GGC	CGG	GAT	GAA	GAT	GGC	CAT	CAC	TCA	GAG	GAG	TCT	TTA	432
	Val	Thr	Glu	Gly	Arg	Asp	Glu	Asp	Gly	His	His	Ser	Glu	Glu	Ser	Leu	
			130				135					140					
10	CAC	TAT	GAG	GGC	CGC	GCG	GTG	GAT	ATC	ACC	ACC	TCA	GAC	CGT	GAC	CGA	480
	His	Tyr	Glu	Gly	Arg	Ala	Val	Asp	Ile	Thr	Thr	Ser	Asp	Arg	Asp	Arg	
						150					155					160	
15	AAT	AAG	TAT	GGA	CTG	CTG	GCG	CGC	TTA	GCA	GTG	GAG	GCC	GGC	TTC	GAC	528
	Asn	Lys	Tyr	Gly	Leu	Leu	Ala	Arg	Leu	Ala	Val	Glu	Ala	Gly	Phe	Asp	
					165					170					175		
20	TGG	GTG	TAT	TAC	GAG	TCC	AAG	GCC	CAC	GTG	CAT	TGC	TCT	GTC	AAG	TCT	576
	Trp	Val	Tyr	Tyr	Glu	Ser	Lys	Ala	His	Val	His	Cys	Ser	Val	Lys	Ser	
				180					185					190			
25	GAG	CAT	TCG	GCC	GCT	GCC	AAG	ACA	GGT	GGC	TGC	TTT	CCT	GCC	GGA	GCC	624
	Glu	His	Ser	Ala	Ala	Ala	Lys	Thr	Gly	Gly	Cys	Phe	Pro	Ala	Gly	Ala	
				195				200					205				
30	CAG	GTG	CGC	CTA	GAG	AAC	GGG	GAG	CGT	GTG	GCC	CTG	TCA	GCT	GTA	AAG	672
	Gln	Val	Arg	Leu	Glu	Asn	Gly	Glu	Arg	Val	Ala	Leu	Ser	Ala	Val	Lys	
				210			215					220					
35	CCA	GGA	GAC	CGG	GTG	CTG	GCC	ATG	GGG	GAG	GAT	GGG	ACC	CCC	ACC	TTC	720
	Pro	Gly	Asp	Arg	Val	Leu	Ala	Met	Gly	Glu	Asp	Gly	Thr	Pro	Thr	Phe	
						230					235					240	
40	AGT	GAT	GTG	CTT	ATT	TTC	CTG	GAC	CGC	GAG	CCA	AAC	CGG	CTG	AGA	GCT	768
	Ser	Asp	Val	Leu	Ile	Phe	Leu	Asp	Arg	Glu	Pro	Asn	Arg	Leu	Arg	Ala	
					245					250					255		
45	TTC	CAG	GTC	ATC	GAG	ACT	CAG	GAT	CCT	CCG	CGT	CGG	CTG	GCG	CTC	ACG	816
	Phe	Gln	Val	Ile	Glu	Thr	Gln	Asp	Pro	Pro	Arg	Arg	Leu	Ala	Leu	Thr	
				260					265					270			
50	CCT	GCC	CAC	CTG	CTC	TTC	ATT	GCG	GAC	AAT	CAT	ACA	GAA	CCA	GCA	GCC	864
	Pro	Ala	His	Leu	Leu	Phe	Ile	Ala	Asp	Asn	His	Thr	Glu	Pro	Ala	Ala	
				275				280					285				
55	CAC	TTC	CGG	GCC	ACA	TTT	GCC	AGC	CAT	GTG	CAA	CCA	GGC	CAA	TAT	GTG	912
	His	Phe	Arg	Ala	Thr	Phe	Ala	Ser	His	Val	Gln	Pro	Gly	Gln	Tyr	Val	
				290			295					300					
60	CTG	GTA	TCA	GGG	GTA	CCA	GGC	CTC	CAG	CCT	GCT	CGG	GTG	GCA	GCT	GTC	960
	Leu	Val	Ser	Gly	Val	Pro	Gly	Leu	Gln	Pro	Ala	Arg	Val	Ala	Ala	Val	
				305		310					315					320	
65	TCC	ACC	CAC	GTG	GCC	CTT	GGG	TCC	TAT	GCT	CCT	CTC	ACA	AGG	CAT	GGG	1008
	Ser	Thr	His	Val	Ala	Leu	Gly	Ser	Tyr	Ala	Pro	Leu	Thr	Arg	His	Gly	
				325						330					335		
70	ACA	CTT	GTG	GTG	GAG	GAT	GTG	GTG	GCC	TCC	TGC	TTT	GCA	GCT	GTG	GCT	1056
	Thr	Leu	Val	Val	Glu	Asp	Val	Val	Ala	Ser	Cys	Phe	Ala	Ala	Val	Ala	

	340	345	350	
5	GAC CAC CAT CTG GCT CAG TTG GCC TTC TGG CCC CTG CGA CTG TTT CCC Asp His His Leu Ala Gln Leu Ala Phe Trp Pro Leu Arg Leu Phe Pro 355 360 365			1104
10	AGT TTG GCA TGG GGC AGC TGG ACC CCA AGT GAG GGT GTT CAC TCC TAC Ser Leu Ala Trp Gly Ser Trp Thr Pro Ser Glu Gly Val His Ser Tyr 370 375 380			1152
15	CCT CAG ATG CTC TAC CGC CTG GGG CGT CTC TTG CTA GAA GAG AGC ACC Pro Gln Met Leu Tyr Arg Leu Gly Arg Leu Leu Glu Glu Ser Thr 385 390 395 400			1200
20	TTC CAT CCA CTG GGC ATG TCT GGG GCA GGA AGC TGAAGGGACT CTAACCACTG Phe His Pro Leu Gly Met Ser Gly Ala Gly Ser 405 410			1253
	CCCTCCTGGA ACTGCTGTGC GTGGATCC			1281
(2) INFORMATION FOR SEQ ID NO:4:				
25	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1313 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: linear			
30	(ii) MOLECULE TYPE: cDNA			
35	(ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 1..1314			
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:			
40	ATG CTG CTG CTG CTG GCC AGA TGT TTT CTG GTG ATC CTT GCT TCC TCG Met Leu Leu Leu Leu Ala Arg Cys Phe Leu Val Ile Leu Ala Ser Ser 1 5 10 15			48
45	CTG CTG GTG TGC CCC GGG CTG GCC TGT GGG CCC GGC AGG GGG TTT GGA Leu Leu Val Cys Pro Gly Leu Ala Cys Gly Pro Gly Arg Gly Phe Gly 20 25 30			96
50	AAG AGG CGG CAC CCC AAA AAG CTG ACC CCT TTA GCC TAC AAG CAG TTT Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys Gln Phe 35 40 45			144
55	ATT CCC AAC GTA GCC GAG AAG ACC CTA GGG GCC AGC GGC AGA TAT GAA Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg Tyr Glu 50 55 60			192
	GGG AAG ATC ACA AGA AAC TCC GAA CGA TTT AAG GAA CTC ACC CCC AAT Gly Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr Pro Asn 65 70 75 80			240

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		TAC AAC CCC GAC ATC ATA TTT AAG GAT GAG GAA AAC ACG GGA GCA GAC	288
		Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Asn Thr Gly Ala Asp	
		85 90 95	
5		CGG CTG ATG ACT CAG AGG TGC AAA GAC AAG TTA AAT GCC TTG GCC ATC	336
		Arg Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ala Leu Ala Ile	
		100 105 110	
10		TCT GTG ATG AAC CAG TGG CCT GGA GTG AGG CTG CGA GTG ACC GAG GGC	384
		Ser Val Met Asn Gln Trp Pro Gly Val Arg Leu Arg Val Thr Glu Gly	
		115 120 125	
15		TGG GAT GAG GAC GGC CAT CAT TCA GAG GAG TCT CTA CAC TAT GAG GGT	432
		Trp Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr Glu Gly	
		130 135 140	
20		CGA GCA GTG GAC ATC ACC ACG TCC GAC CGG GAC CGC AGC AAG TAC GGC	480
		Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg Ser Lys Tyr Gly	
		145 150 155 160	
25		ATG CTG GCT CGC CTG GCT GTG GAA GCA GGT TTC GAC TGG GTC TAC TAT	528
		Met Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr	
		165 170 175	
30		GAA TCC AAA GCT CAC ATC CAC TGT TCT GTG AAA GCA GAG AAC TCC GTG	576
		Glu Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn Ser Val	
		180 185 190	
35		GCG GCC AAA TCC GGC GGC TGT TTC CCG GGA TCC GCC ACC GTG CAC CTG	624
		Ala Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Thr Val His Leu	
		195 200 205	
40		GAG CAG GGC GGC ACC AAG CTG GTG AAG GAC TTA CGT CCC GGA GAC CGC	672
		Glu Gln Gly Gly Thr Lys Leu Val Lys Asp Leu Arg Pro Gly Asp Arg	
		210 215 220	
45		GTG CTG GCG GCT GAC GAC CAG GGC CGG CTG CTG TAC AGC GAC TTC CTC	720
		Val Leu Ala Ala Asp Asp Gln Gly Arg Leu Leu Tyr Ser Asp Phe Leu	
		225 230 235 240	
50		ACC TTC CTG GAC CGC GAC GAA GGC GCC AAG AAG GTC TTC TAC GTG ATC	768
		Thr Phe Leu Asp Arg Asp Glu Gly Ala Lys Lys Val Phe Tyr Val Ile	
		245 250 255	
55		GAG ACG CTG GAG CCG CGC GAG CGC CTG CTG CTC ACC GCC GCG CAC CTG	816
		Glu Thr Leu Glu Pro Arg Glu Arg Leu Leu Leu Thr Ala Ala His Leu	
		260 265 270	
60		CTC TTC GTG GCG CCG CAC AAC GAC TCG GGG CCC ACG CCC GGG CCA AGC	864
		Leu Phe Val Ala Pro His Asn Asp Ser Gly Pro Thr Pro Gly Pro Ser	
		275 280 285	
65		GCG CTC TTT GCC AGC CGC GTG CGC CCC GGG CAG CGC GTG TAC GTG GTG	912
		Ala Leu Phe Ala Ser Arg Val Arg Pro Gly Gln Arg Val Tyr Val Val	
		290 295 300	
70		GCT GAA CGC GGC GGG GAC CGC CGG CTG CTG CCC GCC GCG GTG CAC AGC	960

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Ala Glu Arg Gly Gly Asp Arg Arg Leu Leu Pro Ala Ala Val His Ser
305 310 315 320

5 GTG ACG CTG CGA GAG GAG GAG GCG GGC GCG TAC GCG CCG CTC ACG GCG 1008
Val Thr Leu Arg Glu Glu Glu Ala Gly Ala Tyr Ala Pro Leu Thr Ala
325 330 335

10 CAC GGC ACC ATT CTC ATC AAC CGG GTG CTC GCC TCG TGC TAC GCT GTC 1056
His Gly Thr Ile Leu Ile Asn Arg Val Leu Ala Ser Cys Tyr Ala Val
340 345 350

15 ATC GAG GAG CAC AGC TGG GCA CAC CGG GCC TTC GCG CCT TTC CGC CTG 1104
Ile Glu Glu His Ser Trp Ala His Arg Ala Phe Ala Pro Phe Arg Leu
355 360 365

GCG CAC GCG CTG CTG GCC GCG CTG GCA CCC GCC CGC ACG GAC GGC GGG 1152
Ala His Ala Leu Leu Ala Ala Leu Ala Pro Ala Arg Thr Asp Gly Gly
370 375 380

20 GGC GGG GGC AGC ATC CCT GCA GCG CAA TCT GCA ACG GAA GCG AGG GGC 1200
Gly Gly Gly Ser Ile Pro Ala Ala Gln Ser Ala Thr Glu Ala Arg Gly
385 390 395 400

25 GCG GAG CCG ACT GCG GGC ATC CAC TGG TAC TCG CAG CTG CTC TAC CAC 1248
Ala Glu Pro Thr Ala Gly Ile His Trp Tyr Ser Gln Leu Leu Tyr His
405 410 415

30 ATT GGC ACC TGG CTG TTG GAC AGC GAG ACC ATG CAT CCC TTG GGA ATG 1296
Ile Gly Thr Trp Leu Leu Asp Ser Glu Thr Met His Pro Leu Gly Met
420 425 430

35 GCG GTC AAG TCC AGC TG 1313
Ala Val Lys Ser Ser
435

(2) INFORMATION FOR SEQ ID NO:5:

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1256 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: cDNA

50 (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..1257

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

55 ATG CGG CTT TTG ACG AGA GTG CTG CTG GTG TCT CTT CTC ACT CTG TCC 48
Met Arg Leu Leu Thr Arg Val Leu Leu Val Ser Leu Leu Thr Leu Ser
1 5 10 15

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	TTG GTG GTG TCC GGA CTG GCC TGC GGT CCT GGC AGA GGC TAC GGC AGA	96
	Leu Val Val Ser Gly Leu Ala Cys Gly Pro Gly Arg Gly Tyr Gly Arg	
	20 25 30	
5	AGA AGA CAT CCG AAG AAG CTG ACA CCT CTC GCC TAC AAG CAG TTC ATA	144
	Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys Gln Phe Ile	
	35 40 45	
10	CCT AAT GTC GCG GAG AAG ACC TTA GGG GCC AGC GGC AGA TAC GAG GGC	192
	Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg Tyr Glu Gly	
	50 55 60	
15	AAG ATA ACG CGC AAT TCG GAG AGA TTT AAA GAA CTT ACT CCA AAT TAC	240
	Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr Pro Asn Tyr	
	65 70 75 80	
20	AAT CCC GAC ATT ATC TTT AAG GAT GAG GAG AAC ACG GGA GCG GAC AGG	288
	Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly Ala Asp Arg	
	85 90 95	
25	CTC ATG ACA CAG AGA TGC AAA GAC AAG CTG AAC TCG CTG GCC ATC TCT	336
	Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ser Leu Ala Ile Ser	
	100 105 110	
30	GTA ATG AAC CAC TGG CCA GGG GTT AAG CTG CGT GTG ACA GAG GGC TGG	384
	Val Met Asn His Trp Pro Gly Val Lys Leu Arg Val Thr Glu Gly Trp	
	115 120 125	
35	GAT GAG GAC GGT CAC CAT TTT GAA GAA TCA CTC CAC TAC GAG GGA AGA	432
	Asp Glu Asp Gly His His Phe Glu Glu Ser Leu His Tyr Glu Gly Arg	
	130 135 140	
40	GCT GTT GAT ATT ACC ACC TCT GAC CGA GAC AAG AGC AAA TAC GGG ACA	480
	Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Lys Ser Lys Tyr Gly Thr	
	145 150 155 160	
45	CTG TCT CGC CTA GCT GTG GAG GCT GGA TTT GAC TGG GTC TAT TAC GAG	528
	Leu Ser Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr Glu	
	165 170 175	
50	TCC AAA GCC CAC ATT CAT TGC TCT GTC AAA GCA GAA AAT TCG GTT GCT	576
	Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn Ser Val Ala	
	180 185 190	
55	GCG AAA TCT GGG GGC TGT TTC CCA GGT TCG GCT CTG GTC TCG CTC CAG	624
	Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Leu Val Ser Leu Gln	
	195 200 205	
60	GAC GGA GGA CAG AAG GCC GTG AAG GAC CTG AAC CCC GGA GAC AAG GTG	672
	Asp Gly Gly Gln Lys Ala Val Lys Asp Leu Asn Pro Gly Asp Lys Val	
	210 215 220	
65	CTG GCG GCA GAC AGC GCG GGA AAC CTG GTG TTC AGC GAC TTC ATC ATG	720
	Leu Ala Ala Asp Ser Ala Gly Asn Leu Val Phe Ser Asp Phe Ile Met	
	225 230 235 240	
70	TTC ACA GAC CGA GAC TCC ACG ACG CGA CGT GTG TTT TAC GTC ATA GAA	768
	Phe Thr Asp Arg Asp Ser Thr Thr Arg Arg Val Phe Tyr Val Ile Glu	

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	245	250	255	
5	ACG CAA GAA CCC GTT GAA AAG ATC ACC Thr Gln Glu Pro Val Glu Lys Ile Thr 260	CTC ACC GCC GCT CAC CTC CTT Leu Thr Ala Ala His Leu Leu 265	816	
10	TTT GTC CTC GAC AAC TCA ACG GAA GAT Phe Val Leu Asp Asn Ser Thr Glu Asp 275	CTC CAC ACC ATG ACC GCC GCG Leu His Thr Met Thr Ala Ala 280	864	
15	TAT GCC AGC AGT GTC AGA GCC GGA CAA AAG Tyr Ala Ser Ser Val Arg Ala Gly Gln Lys 290	GTG ATG GTT GTT GAT GAT Val Met Val Val Asp Asp 300	912	
20	AGC GGT CAG CTT AAA TCT GTC ATC GTG Ser Gly Gln Leu Lys Ser Val Ile Val 305	CAG CGG ATA TAC ACG GAG GAG Gln Arg Ile Tyr Thr Glu Glu 310	960	
25	CAG CGG GGC TCG TTC GCA CCA GTG ACT Gln Arg Gly Ser Phe Ala Pro Val Thr 325	GCA CAT GGG ACC ATT GTG GTC Ala His Gly Thr Ile Val Val 330	1008	
30	GAC AGA ATA CTG GCG TCC TGT TAC GCC Asp Arg Ile Leu Ala Ser Cys Tyr Ala 340	GTA ATA GAG GAC CAG GGG CTT Val Ile Glu Asp Gln Gly Leu 345	1056	
35	GCG CAT TTG GCC TTC GCG CCC GCC AGG Ala His Leu Ala Phe Ala Pro Ala Arg 355	CTC TAT TAT TAC GTG TCA TCA Leu Tyr Tyr Tyr Val Ser Ser 360	1104	
40	TTC CTG TCC CCC AAA ACT CCA GCA GTC Phe Leu Ser Pro Lys Thr Pro Ala Val 370	GGT CCA ATG CGA CTT TAC AAC Gly Pro Met Arg Leu Tyr Asn 375	1152	
45	AGG AGG GGG TCC ACT GGT ACT CCA GGC Arg Arg Gly Ser Thr Gly Thr Pro Gly 385	TCC TGT CAT CAA ATG GGA ACG Ser Cys His Gln Met Gly Thr 390	1200	
50	TGG CTT TTG GAC AGC AAC ATG CTT CAT Trp Leu Leu Asp Ser Asn Met Leu His 405	CCT TTG GGG ATG TCA GTA AAC Pro Leu Gly Met Ser Val Asn 410	1248	
55	TCA AGC TG Ser Ser		1256	

(2) INFORMATION FOR SEQ ID NO:6:

- 50 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1425 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- 55 (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..1425

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

10	ATG CTG CTG CTG GCG AGA TGT CTG CTG CTA GTC CTC GTC TCC TCG CTG	48
	Met Leu Leu Leu Ala Arg Cys Leu Leu Leu Val Leu Val Ser Ser Leu	
	1 5 10 15	
15	CTG GTA TGC TCG GGA CTG GCG TGC GGA CCG GGC AGG GGG TTC GGG AAG	96
	Leu Val Cys Ser Gly Leu Ala Cys Gly Pro Gly Arg Gly Phe Gly Lys	
	20 25 30	
20	AGG AGG CAC CCC AAA AAG CTG ACC CCT TTA GCC TAC AAG CAG TTT ATC	144
	Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys Gln Phe Ile	
	35 40 45	
25	CCC AAT GTG GCC GAG AAG ACC CTA GGC GCC AGC GGA AGG TAT GAA GGG	192
	Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg Tyr Glu Gly	
	50 55 60	
30	AAG ATC TCC AGA AAC TCC GAG CGA TTT AAG GAA CTC ACC CCC AAT TAC	240
	Lys Ile Ser Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr Pro Asn Tyr	
	65 70 75 80	
35	AAC CCC GAC ATC ATA TTT AAG GAT GAA GAA AAC ACC GGA GCG GAC AGG	288
	Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly Ala Asp Arg	
	85 90 95	
40	CTG ATG ACT CAG AGG TGT AAG GAC AAG TTG AAC GCT TTG GCC ATC TCG	336
	Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ala Leu Ala Ile Ser	
	100 105 110	
45	GTG ATG AAC CAG TGG CCA GGA GTG AAA CTG CGG GTG ACC GAG GGC TGG	384
	Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg Val Thr Glu Gly Trp	
	115 120 125	
50	GAC GAA GAT GGC CAC CAC TCA GAG GAG TCT CTG CAC TAC GAG GGC CGC	432
	Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr Glu Gly Arg	
	130 135 140	
55	GCA GTG GAC ATC ACC ACG TCT GAC CGC GAC CGC AGC AAG TAC GGC ATG	480
	Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg Ser Lys Tyr Gly Met	
	145 150 155 160	
60	CTG GCC CGC CTG GCG GTG GAG GCC GGC TTC GAC TGG GTG TAC TAC GAG	528
	Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr Glu	
	165 170 175	
65	TCC AAG GCA CAT ATC CAC TGC TCG GTG AAA GCA GAG AAC TCG GTG GCG	576
	Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn Ser Val Ala	
	180 185 190	
70	GCC AAA TCG GGA GGC TGC TTC CCG GGC TCG GCC ACG GTG CAC CTG GAG	624
	Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Thr Val His Leu Glu	
	195 200 205	

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		CAG	GGC	GGC	ACC	AAG	CTG	GTG	AAG	GAC	CTG	AGC	CCC	GGG	GAC	CGC	GTG	672
		Gln	Gly	Gly	Thr	Lys	Leu	Val	Lys	Asp	Leu	Ser	Pro	Gly	Asp	Arg	Val	
		210						215					220					
5		CTG	GCG	GCG	GAC	GAC	CAG	GGC	CGG	CTG	CTC	TAC	AGC	GAC	TTC	CTC	ACT	720
		Leu	Ala	Ala	Asp	Asp	Gln	Gly	Arg	Leu	Leu	Tyr	Ser	Asp	Phe	Leu	Thr	
		225					230					235					240	
10		TTC	CTG	GAC	CGC	GAC	GAC	GGC	GCC	AAG	AAG	GTC	TTC	TAC	GTG	ATC	GAG	768
		Phe	Leu	Asp	Arg	Asp	Asp	Gly	Ala	Lys	Lys	Val	Phe	Tyr	Val	Ile	Glu	
						245					250					255		
15		ACG	CGG	GAG	CCG	CGC	GAG	CGC	CTG	CTG	CTC	ACC	GCC	GCG	CAC	CTG	CTC	816
		Thr	Arg	Glu	Pro	Arg	Glu	Arg	Leu	Leu	Leu	Thr	Ala	Ala	His	Leu	Leu	
					260					265					270			
20		TTT	GTG	GCG	CCG	CAC	AAC	GAC	TCG	GCC	ACC	GGG	GAG	CCC	GAG	GCG	TCC	864
		Phe	Val	Ala	Pro	His	Asn	Asp	Ser	Ala	Thr	Gly	Glu	Pro	Glu	Ala	Ser	
				275					280					285				
25		TCG	GGC	TCG	GGG	CCG	CCT	TCC	GGG	GGC	GCA	CTG	GGG	CCT	CGG	GCG	CTG	912
		Ser	Gly	Ser	Gly	Pro	Pro	Ser	Gly	Gly	Ala	Leu	Gly	Pro	Arg	Ala	Leu	
		290						295					300					
30		TTC	GCC	AGC	CGC	GTG	CGC	CCG	GGC	CAG	CGC	GTG	TAC	GTG	GTG	GCC	GAG	960
		Phe	Ala	Ser	Arg	Val	Arg	Pro	Gly	Gln	Arg	Val	Tyr	Val	Val	Ala	Glu	
		305					310					315					320	
35		CGT	GAC	GGG	GAC	CGC	CGG	CTC	CTG	CCC	GCC	GCT	GTG	CAC	AGC	GTG	ACC	1008
		Arg	Asp	Gly	Asp	Arg	Arg	Leu	Leu	Pro	Ala	Ala	Val	His	Ser	Val	Thr	
						325					330					335		
40		CTA	AGC	GAG	GAG	GCC	GCG	GGC	GCC	TAC	GCG	CCG	CTC	ACG	GCC	CAG	GGC	1056
		Leu	Ser	Glu	Glu	Ala	Ala	Gly	Ala	Tyr	Ala	Pro	Leu	Thr	Ala	Gln	Gly	
					340					345					350			
45		ACC	ATT	CTC	ATC	AAC	CGG	GTG	CTG	GCC	TCG	TGC	TAC	GCG	GTC	ATC	GAG	1104
		Thr	Ile	Leu	Ile	Asn	Arg	Val	Leu	Ala	Ser	Cys	Tyr	Ala	Val	Ile	Glu	
				355					360					365				
50		GAG	CAC	AGC	TGG	GCG	CAC	CGG	GCC	TTC	GCG	CCC	TTC	CGC	CTG	GCG	CAC	1152
		Glu	His	Ser	Trp	Ala	His	Arg	Ala	Phe	Ala	Pro	Phe	Arg	Leu	Ala	His	
			370					375					380					
55		GCG	CTC	CTG	GCT	GCA	CTG	GCG	CCC	GCG	CGC	ACG	GAC	CGC	GGC	GGG	GAC	1200
		Ala	Leu	Leu	Ala	Ala	Leu	Ala	Pro	Ala	Arg	Thr	Asp	Arg	Gly	Gly	Asp	
		385					390					395					400	
60		AGC	GGC	GGC	GGG	GAC	CGC	GGG	GGC	GGC	GGC	GGC	AGA	GTA	GCC	CTA	ACC	1248
		Ser	Gly	Gly	Gly	Asp	Arg	Gly	Gly	Gly	Gly	Gly	Arg	Val	Ala	Leu	Thr	
						405					410					415		
65		GCT	CCA	GGT	GCT	GCC	GAC	GCT	CCG	GGT	GCG	GGG	GCC	ACC	GCG	GGC	ATC	1296
		Ala	Pro	Gly	Ala	Ala	Asp	Ala	Pro	Gly	Ala	Gly	Ala	Thr	Ala	Gly	Ile	
				420						425					430			
70		CAC	TGG	TAC	TCG	CAG	CTG	CTC	TAC	CAA	ATA	GGC	ACC	TGG	CTC	CTG	GAC	1344

His Trp Tyr Ser Gln Leu Leu Tyr Gln Ile Gly Thr Trp Leu Leu Asp
435 440 445

5 AGC GAG GCC CTG CAC CCG CTG GGC ATG GCG GTC AAG TCC AGC NNN AGC 1392
Ser Glu Ala Leu His Pro Leu Gly Met Ala Val Lys Ser Ser Xaa Ser
450 455 460

10 CGG GGG GCC GGG GGA GGG GCG CGG GAG GGG GCC 1425
Arg Gly Ala Gly Gly Gly Ala Arg Glu Gly Ala
465 470 475

(2) INFORMATION FOR SEQ ID NO:7:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 939 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
20 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

25 (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..939

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CGG CGC CTC ATG ACC CAG CGC TGC AAG GAC CGC CTG AAC TCG CTG GCT 48
Arg Arg Leu Met Thr Gln Arg Cys Lys Asp Arg Leu Asn Ser Leu Ala
1 5 10 15

35 ATC TCG GTG ATG AAC CAG TGG CCC GGT GTG AAG CTG CGG GTG ACC GAG 96
Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg Val Thr Glu
20 25 30

40 GGC TGG GAC GAG GAC GGC CAC CAC TCA GAG GAG TCC CTG CAT TAT GAG 144
Gly Trp Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr Glu
35 40 45

45 GGC CGC GCG GTG GAC ATC ACC ACA TCA GAC CGC GAC CGC AAT AAG TAT 192
Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg Asn Lys Tyr
50 55 60

50 GGA CTG CTG GCG CGC TTG GCA GTG GAG GCC GGC TTT GAC TGG GTG TAT 240
Gly Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr
65 70 75 80

TAC GAG TCA AAG GCC CAC GTG CAT TGC TCC GTC AAG TCC GAG CAC TCG 288
Tyr Glu Ser Lys Ala His Val His Cys Ser Val Lys Ser Glu His Ser
85 90 95

55 GCC GCA GCC AAG ACG GGC GGC TGC TTC CCT GCC GGA GCC CAG GTA CGC 336
Ala Ala Ala Lys Thr Gly Gly Cys Phe Pro Ala Gly Ala Gln Val Arg
100 105 110

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	CTG GAG AGT GGG GCG CGT GTG GCC TTG TCA GCC GTG AGG CCG GGA GAC	384
	Leu Glu Ser Gly Ala Arg Val Ala Leu Ser Ala Val Arg Pro Gly Asp	
	115 120 125	
5	CGT GTG CTG GCC ATG GGG GAG GAT GGG AGC CCC ACC TTC AGC GAT GTG	432
	Arg Val Leu Ala Met Gly Glu Asp Gly Ser Pro Thr Phe Ser Asp Val	
	130 135 140	
10	CTC ATT TTC CTG GAC CGC GAG CCC CAC AGG CTG AGA GCC TTC CAG GTC	480
	Leu Ile Phe Leu Asp Arg Glu Pro His Arg Leu Arg Ala Phe Gln Val	
	145 150 155 160	
15	ATC GAG ACT CAG GAC CCC CCA CGC CGC CTG GCA CTC ACA CCC GCT CAC	528
	Ile Glu Thr Gln Asp Pro Pro Arg Arg Leu Ala Leu Thr Pro Ala His	
	165 170 175	
20	CTG CTC TTT ACG GCT GAC AAT CAC ACG GAG CCG GCA GCC CGC TTC CGG	576
	Leu Leu Phe Thr Ala Asp Asn His Thr Glu Pro Ala Ala Arg Phe Arg	
	180 185 190	
25	GCC ACA TTT GCC AGC CAC GTG CAG CCT GGC CAG TAC GTG CTG GTG GCT	624
	Ala Thr Phe Ala Ser His Val Gln Pro Gly Gln Tyr Val Leu Val Ala	
	195 200 205	
30	GGG GTG CCA GGC CTG CAG CCT GCC CGC GTG GCA GCT GTC TCT ACA CAC	672
	Gly Val Pro Gly Leu Gln Pro Ala Arg Val Ala Ala Val Ser Thr His	
	210 215 220	
35	GTG GCC CTC GGG GCC TAC GCC CCG CTC ACA AAG CAT GGG ACA CTG GTG	720
	Val Ala Leu Gly Ala Tyr Ala Pro Leu Thr Lys His Gly Thr Leu Val	
	225 230 235 240	
40	GTG GAG GAT GTG GTG GCA TCC TGC TTC GCG GCC GTG GCT GAC CAC CAC	768
	Val Glu Asp Val Val Ala Ser Cys Phe Ala Ala Val Ala Asp His His	
	245 250 255	
45	CTG GCT CAG TTG GCC TTC TGG CCC CTG AGA CTC TTT CAC AGC TTG GCA	816
	Leu Ala Gln Leu Ala Phe Trp Pro Leu Arg Leu Phe His Ser Leu Ala	
	260 265 270	
50	TGG GGC AGC TGG ACC CCG GGG GAG GGT GTG CAT TGG TAC CCC CAG CTG	864
	Trp Gly Ser Trp Thr Pro Gly Glu Gly Val His Trp Tyr Pro Gln Leu	
	275 280 285	
55	CTC TAC CGC CTG GGG CGT CTC CTG CTA GAA GAG GGC AGC TTC CAC CCA	912
	Leu Tyr Arg Leu Gly Arg Leu Leu Leu Glu Glu Gly Ser Phe His Pro	
	290 295 300	
60	CTG GGC ATG TCC GGG GCA GGG AGC TGA	939
	Leu Gly Met Ser Gly Ala Gly Ser Xaa	
	305 310	

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 425 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

10 Met Val Glu Met Leu Leu Leu Thr Arg Ile Leu Leu Val Gly Phe Ile
1 5 10 15

Cys Ala Leu Leu Val Ser Ser Gly Leu Thr Cys Gly Pro Gly Arg Gly
20 25 30

15 Ile Gly Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys
35 40 45

Gln Phe Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg
50 55 60

20 Tyr Glu Gly Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr
65 70 75 80

25 Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly
85 90 95

Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ala Leu
100 105 110

30 Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg Val Thr
115 120 125

Glu Gly Trp Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr
130 135 140

35 Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg Ser Lys
145 150 155 160

40 Tyr Gly Met Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val
165 170 175

Tyr Tyr Glu Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn
180 185 190

45 Ser Val Ala Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Thr Val
195 200 205

His Leu Glu His Gly Gly Thr Lys Leu Val Lys Asp Leu Ser Pro Gly
210 215 220

50 Asp Arg Val Leu Ala Ala Asp Ala Asp Gly Arg Leu Leu Tyr Ser Asp
225 230 235 240

Phe Leu Thr Phe Leu Asp Arg Met Asp Ser Ser Arg Lys Leu Phe Tyr
245 250 255

Val Ile Glu Thr Arg Gln Pro Arg Ala Arg Leu Leu Leu Thr Ala Ala
260 265 270

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His Leu Leu Phe Val Ala Pro Gln His Asn Gln Ser Glu Ala Thr Gly
275 280 285

5 Ser Thr Ser Gly Gln Ala Leu Phe Ala Ser Asn Val Lys Pro Gly Gln
290 295 300

Arg Val Tyr Val Leu Gly Glu Gly Gly Gln Gln Leu Leu Pro Ala Ser
305 310 315 320

10 Val His Ser Val Ser Leu Arg Glu Glu Ala Ser Gly Ala Tyr Ala Pro
325 330 335

Leu Thr Ala Gln Gly Thr Ile Leu Ile Asn Arg Val Leu Ala Ser Cys
15 340 345 350

Tyr Ala Val Ile Glu Glu His Ser Trp Ala His Trp Ala Phe Ala Pro
355 360 365

20 Phe Arg Leu Ala Gln Gly Leu Leu Ala Ala Leu Cys Pro Asp Gly Ala
370 375 380

Ile Pro Thr Ala Ala Thr Thr Thr Thr Gly Ile His Trp Tyr Ser Arg
25 385 390 395 400

Leu Leu Tyr Arg Ile Gly Ser Trp Val Leu Asp Gly Asp Ala Leu His
405 410 415

30 Pro Leu Gly Met Val Ala Pro Ala Ser
420 425

(2) INFORMATION FOR SEQ ID NO:9:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 396 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

45 Met Ala Leu Pro Ala Ser Leu Leu Pro Leu Cys Cys Leu Ala Leu Leu
1 5 10 15

Ala Leu Ser Ala Gln Ser Cys Gly Pro Gly Arg Gly Pro Val Gly Arg
50 20 25 30

Arg Arg Tyr Val Arg Lys Gln Leu Val Pro Leu Leu Tyr Lys Gln Phe
35 40 45

55 Val Pro Ser Met Pro Glu Arg Thr Leu Gly Ala Ser Gly Pro Ala Glu
50 55 60

Gly Arg Val Thr Arg Gly Ser Glu Arg Phe Arg Asp Leu Val Pro Asn

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	65		70		75		80									
	Tyr	Asn	Pro	Asp	Ile	Ile	Phe	Lys	Asp	Glu	Glu	Asn	Ser	Gly	Ala	Asp
					85					90					95	
5	Arg	Leu	Met	Thr	Glu	Arg	Cys	Lys	Glu	Arg	Val	Asn	Ala	Leu	Ala	Ile
				100					105					110		
	Ala	Val	Met	Asn	Met	Trp	Pro	Gly	Val	Arg	Leu	Arg	Val	Thr	Glu	Gly
10			115					120					125			
	Trp	Asp	Glu	Asp	Gly	His	His	Ala	Gln	Asp	Ser	Leu	His	Tyr	Glu	Gly
	130					135						140				
15	Arg	Ala	Leu	Asp	Ile	Thr	Thr	Ser	Asp	Arg	Asp	Arg	Asn	Lys	Tyr	Gly
	145				150						155					160
	Leu	Leu	Ala	Arg	Leu	Ala	Val	Glu	Ala	Gly	Phe	Asp	Trp	Val	Tyr	Tyr
				165						170					175	
20	Glu	Ser	Arg	Asn	His	Ile	His	Val	Ser	Val	Lys	Ala	Asp	Asn	Ser	Leu
				180					185					190		
	Ala	Val	Arg	Ala	Gly	Gly	Cys	Phe	Pro	Gly	Asn	Ala	Thr	Val	Arg	Leu
25			195					200					205			
	Arg	Ser	Gly	Glu	Arg	Lys	Gly	Leu	Arg	Glu	Leu	His	Arg	Gly	Asp	Trp
	210						215					220				
30	Val	Leu	Ala	Ala	Asp	Ala	Ala	Gly	Arg	Val	Val	Pro	Thr	Pro	Val	Leu
	225					230					235				240	
	Leu	Phe	Leu	Asp	Arg	Asp	Leu	Gln	Arg	Arg	Ala	Ser	Phe	Val	Ala	Val
				245					250					255		
35	Glu	Thr	Glu	Arg	Pro	Pro	Arg	Lys	Leu	Leu	Leu	Thr	Pro	Trp	His	Leu
				260					265					270		
	Val	Phe	Ala	Ala	Arg	Gly	Pro	Ala	Pro	Ala	Pro	Gly	Asp	Phe	Ala	Pro
40			275					280					285			
	Val	Phe	Ala	Arg	Arg	Leu	Arg	Ala	Gly	Asp	Ser	Val	Leu	Ala	Pro	Gly
	290					295						300				
45	Gly	Asp	Ala	Leu	Gln	Pro	Ala	Arg	Val	Ala	Arg	Val	Ala	Arg	Glu	Glu
	305				310					315					320	
	Ala	Val	Gly	Val	Phe	Ala	Pro	Leu	Thr	Ala	His	Gly	Thr	Leu	Leu	Val
				325					330					335		
50	Asn	Asp	Val	Leu	Ala	Ser	Cys	Tyr	Ala	Val	Leu	Glu	Ser	His	Gln	Trp
			340						345					350		
	Ala	His	Arg	Ala	Phe	Ala	Pro	Leu	Arg	Leu	Leu	His	Ala	Leu	Gly	Ala
55			355					360					365			
	Leu	Leu	Pro	Gly	Gly	Ala	Val	Gln	Pro	Thr	Gly	Met	His	Trp	Tyr	Ser
	370					375					380					

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Arg Leu Leu Tyr Arg Leu Ala Glu Glu Leu Met Gly
385 390 395

5

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

10

(A) LENGTH: 411 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

20 Met Ser Pro Ala Trp Leu Arg Pro Arg Leu Arg Phe Cys Leu Phe Leu
1 5 10 15
Leu Leu Leu Leu Leu Val Pro Ala Ala Arg Gly Cys Gly Pro Gly Arg
20 25 30
25 Val Val Gly Ser Arg Arg Arg Pro Pro Arg Lys Leu Val Pro Leu Ala
35 40 45
Tyr Lys Gln Phe Ser Pro Asn Val Pro Glu Lys Thr Leu Gly Ala Ser
50 55 60
30 Gly Arg Tyr Glu Gly Lys Ile Ala Arg Ser Ser Glu Arg Phe Lys Glu
65 70 75 80
Leu Thr Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn
35 85 90 95
Thr Gly Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Arg Leu Asn
100 105 110
40 Ser Leu Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg
115 120 125
Val Thr Glu Gly Arg Asp Glu Asp Gly His His Ser Glu Glu Ser Leu
130 135 140
45 His Tyr Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg
145 150 155 160
Asn Lys Tyr Gly Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp
50 165 170 175
Trp Val Tyr Tyr Glu Ser Lys Ala His Val His Cys Ser Val Lys Ser
180 185 190
55 Glu His Ser Ala Ala Ala Lys Thr Gly Gly Cys Phe Pro Ala Gly Ala
195 200 205
Gln Val Arg Leu Glu Asn Gly Glu Arg Val Ala Leu Ser Ala Val Lys

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210 215 220

Pro Gly Asp Arg Val Leu Ala Met Gly Glu Asp Gly Thr Pro Thr Phe
225 230 235 240

5 Ser Asp Val Leu Ile Phe Leu Asp Arg Glu Pro Asn Arg Leu Arg Ala
245 250 255

10 Phe Gln Val Ile Glu Thr Gln Asp Pro Pro Arg Arg Leu Ala Leu Thr
260 265 270

Pro Ala His Leu Leu Phe Ile Ala Asp Asn His Thr Glu Pro Ala Ala
275 280 285

15 His Phe Arg Ala Thr Phe Ala Ser His Val Gln Pro Gly Gln Tyr Val
290 295 300

Leu Val Ser Gly Val Pro Gly Leu Gln Pro Ala Arg Val Ala Ala Val
305 310 315 320

20 Ser Thr His Val Ala Leu Gly Ser Tyr Ala Pro Leu Thr Arg His Gly
325 330 335

25 Thr Leu Val Val Glu Asp Val Val Ala Ser Cys Phe Ala Ala Val Ala
340 345 350

Asp His His Leu Ala Gln Leu Ala Phe Trp Pro Leu Arg Leu Phe Pro
355 360 365

30 Ser Leu Ala Trp Gly Ser Trp Thr Pro Ser Glu Gly Val His Ser Tyr
370 375 380

Pro Gln Met Leu Tyr Arg Leu Gly Arg Leu Leu Leu Glu Glu Ser Thr
385 390 395 400

35 Phe His Pro Leu Gly Met Ser Gly Ala Gly Ser
405 410

40 (2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 437 amino acids

(B) TYPE: amino acid

45 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Leu Leu Leu Leu Ala Arg Cys Phe Leu Val Ile Leu Ala Ser Ser
1 5 10 15

55 Leu Leu Val Cys Pro Gly Leu Ala Cys Gly Pro Gly Arg Gly Phe Gly
20 25 30

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Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys Gln Phe
 35 40 45
 5 Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg Tyr Glu
 50 55 60
 Gly Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr Pro Asn
 65 70 75 80
 10 Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly Ala Asp
 85 90 95
 Arg Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ala Leu Ala Ile
 100 105 110
 15 Ser Val Met Asn Gln Trp Pro Gly Val Arg Leu Arg Val Thr Glu Gly
 115 120 125
 20 Trp Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr Glu Gly
 130 135 140
 Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg Ser Lys Tyr Gly
 145 150 155 160
 25 Met Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr
 165 170 175
 Glu Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn Ser Val
 180 185 190
 30 Ala Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Thr Val His Leu
 195 200 205
 Glu Gln Gly Gly Thr Lys Leu Val Lys Asp Leu Arg Pro Gly Asp Arg
 210 215 220
 35 Val Leu Ala Ala Asp Asp Gln Gly Arg Leu Leu Tyr Ser Asp Phe Leu
 225 230 235 240
 40 Thr Phe Leu Asp Arg Asp Glu Gly Ala Lys Lys Val Phe Tyr Val Ile
 245 250 255
 Glu Thr Leu Glu Pro Arg Glu Arg Leu Leu Leu Thr Ala Ala His Leu
 260 265 270
 45 Leu Phe Val Ala Pro His Asn Asp Ser Gly Pro Thr Pro Gly Pro Ser
 275 280 285
 Ala Leu Phe Ala Ser Arg Val Arg Pro Gly Gln Arg Val Tyr Val Val
 290 295 300
 50 Ala Glu Arg Gly Gly Asp Arg Arg Leu Leu Pro Ala Ala Val His Ser
 305 310 315 320
 55 Val Thr Leu Arg Glu Glu Glu Ala Gly Ala Tyr Ala Pro Leu Thr Ala
 325 330 335
 His Gly Thr Ile Leu Ile Asn Arg Val Leu Ala Ser Cys Tyr Ala Val

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340 345 350

Ile Glu Glu His Ser Trp Ala His Arg Ala Phe Ala Pro Phe Arg Leu
355 360 365

5 Ala His Ala Leu Leu Ala Ala Leu Ala Pro Ala Arg Thr Asp Gly Gly
370 375 380

Gly Gly Gly Ser Ile Pro Ala Ala Gln Ser Ala Thr Glu Ala Arg Gly
10 385 390 395 400

Ala Glu Pro Thr Ala Gly Ile His Trp Tyr Ser Gln Leu Leu Tyr His
405 410 415

15 Ile Gly Thr Trp Leu Leu Asp Ser Glu Thr Met His Pro Leu Gly Met
420 425 430

Ala Val Lys Ser Ser
435

20

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 418 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

35 Met Arg Leu Leu Thr Arg Val Leu Leu Val Ser Leu Leu Thr Leu Ser
1 5 10 15

Leu Val Val Ser Gly Leu Ala Cys Gly Pro Gly Arg Gly Tyr Gly Arg
20 25 30

40 Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys Gln Phe Ile
35 40 45

45 Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg Tyr Glu Gly
50 55 60

Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr Pro Asn Tyr
65 70 75 80

50 Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly Ala Asp Arg
85 90 95

Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ser Leu Ala Ile Ser
100 105 110

55 Val Met Asn His Trp Pro Gly Val Lys Leu Arg Val Thr Glu Gly Trp
115 120 125

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Asp Glu Asp Gly His His Phe Glu Glu Ser Leu His Tyr Glu Gly Arg
 130 135 140
 5 Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Lys Ser Lys Tyr Gly Thr
 145 150 155 160
 Leu Ser Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr Glu
 165 170 175
 10 Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn Ser Val Ala
 180 185 190
 Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Leu Val Ser Leu Gln
 195 200 205
 15 Asp Gly Gly Gln Lys Ala Val Lys Asp Leu Asn Pro Gly Asp Lys Val
 210 215 220
 20 Leu Ala Ala Asp Ser Ala Gly Asn Leu Val Phe Ser Asp Phe Ile Met
 225 230 235 240
 Phe Thr Asp Arg Asp Ser Thr Thr Arg Arg Val Phe Tyr Val Ile Glu
 245 250 255
 25 Thr Gln Glu Pro Val Glu Lys Ile Thr Leu Thr Ala Ala His Leu Leu
 260 265 270
 Phe Val Leu Asp Asn Ser Thr Glu Asp Leu His Thr Met Thr Ala Ala
 275 280 285
 30 Tyr Ala Ser Ser Val Arg Ala Gly Gln Lys Val Met Val Val Asp Asp
 290 295 300
 Ser Gly Gln Leu Lys Ser Val Ile Val Gln Arg Ile Tyr Thr Glu Glu
 305 310 315 320
 Gln Arg Gly Ser Phe Ala Pro Val Thr Ala His Gly Thr Ile Val Val
 325 330 335
 40 Asp Arg Ile Leu Ala Ser Cys Tyr Ala Val Ile Glu Asp Gln Gly Leu
 340 345 350
 Ala His Leu Ala Phe Ala Pro Ala Arg Leu Tyr Tyr Tyr Val Ser Ser
 355 360 365
 45 Phe Leu Ser Pro Lys Thr Pro Ala Val Gly Pro Met Arg Leu Tyr Asn
 370 375 380
 Arg Arg Gly Ser Thr Gly Thr Pro Gly Ser Cys His Gln Met Gly Thr
 385 390 395 400
 50 Trp Leu Leu Asp Ser Asn Met Leu His Pro Leu Gly Met Ser Val Asn
 405 410 415
 55 Ser Ser

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(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 475 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Leu Leu Leu Ala Arg Cys Leu Leu Leu Val Leu Val Ser Ser Leu
1 5 10 15

Leu Val Cys Ser Gly Leu Ala Cys Gly Pro Gly Arg Gly Phe Gly Lys
20 25 30

Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys Gln Phe Ile
35 40 45

Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg Tyr Glu Gly
50 55 60

Lys Ile Ser Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr Pro Asn Tyr
65 70 75 80

Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly Ala Asp Arg
85 90 95

Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ala Leu Ala Ile Ser
100 105 110

Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg Val Thr Glu Gly Trp
115 120 125

Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr Glu Gly Arg
130 135 140

Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg Ser Lys Tyr Gly Met
145 150 155 160

Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr Glu
165 170 175

Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn Ser Val Ala
180 185 190

Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Thr Val His Leu Glu
195 200 205

Gln Gly Gly Thr Lys Leu Val Lys Asp Leu Ser Pro Gly Asp Arg Val
210 215 220

Leu Ala Ala Asp Asp Gln Gly Arg Leu Leu Tyr Ser Asp Phe Leu Thr
225 230 235 240

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Phe Leu Asp Arg Asp Asp Gly Ala Lys Lys Val Phe Tyr Val Ile Glu
245 250 255

5 Thr Arg Glu Pro Arg Glu Arg Leu Leu Leu Thr Ala Ala His Leu Leu
260 265 270

Phe Val Ala Pro His Asn Asp Ser Ala Thr Gly Glu Pro Glu Ala Ser
275 280 285

10 Ser Gly Ser Gly Pro Pro Ser Gly Gly Ala Leu Gly Pro Arg Ala Leu
290 295 300

Phe Ala Ser Arg Val Arg Pro Gly Gln Arg Val Tyr Val Val Ala Glu
305 310 315 320

15 Arg Asp Gly Asp Arg Arg Leu Leu Pro Ala Ala Val His Ser Val Thr
325 330 335

20 Leu Ser Glu Glu Ala Ala Gly Ala Tyr Ala Pro Leu Thr Ala Gln Gly
340 345 350

Thr Ile Leu Ile Asn Arg Val Leu Ala Ser Cys Tyr Ala Val Ile Glu
355 360 365

25 Glu His Ser Trp Ala His Arg Ala Phe Ala Pro Phe Arg Leu Ala His
370 375 380

Ala Leu Leu Ala Ala Leu Ala Pro Ala Arg Thr Asp Arg Gly Gly Asp
385 390 395 400

30 Ser Gly Gly Gly Asp Arg Gly Gly Gly Gly Gly Arg Val Ala Leu Thr
405 410 415

Ala Pro Gly Ala Ala Asp Ala Pro Gly Ala Gly Ala Thr Ala Gly Ile
420 425 430

35 His Trp Tyr Ser Gln Leu Leu Tyr Gln Ile Gly Thr Trp Leu Leu Asp
435 440 445

40 Ser Glu Ala Leu His Pro Leu Gly Met Ala Val Lys Ser Ser Xaa Ser
450 455 460

Arg Gly Ala Gly Gly Gly Ala Arg Glu Gly Ala
465 470 475

45

(2) INFORMATION FOR SEQ ID NO:14:

50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 313 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

55 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Arg Arg Leu Met Thr Gln Arg Cys Lys Asp Arg Leu Asn Ser Leu Ala
1 5 10 15

5 Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg Val Thr Glu
20 25 30

Gly Trp Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr Glu
35 40 45

10 Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg Asn Lys Tyr
50 55 60

Gly Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr
15 65 70 75 80

Tyr Glu Ser Lys Ala His Val His Cys Ser Val Lys Ser Glu His Ser
85 90 95

20 Ala Ala Ala Lys Thr Gly Gly Cys Phe Pro Ala Gly Ala Gln Val Arg
100 105 110

Leu Glu Ser Gly Ala Arg Val Ala Leu Ser Ala Val Arg Pro Gly Asp
115 120 125

25 Arg Val Leu Ala Met Gly Glu Asp Gly Ser Pro Thr Phe Ser Asp Val
130 135 140

Leu Ile Phe Leu Asp Arg Glu Pro His Arg Leu Arg Ala Phe Gln Val
30 145 150 155 160

Ile Glu Thr Gln Asp Pro Pro Arg Arg Leu Ala Leu Thr Pro Ala His
165 170 175

35 Leu Leu Phe Thr Ala Asp Asn His Thr Glu Pro Ala Ala Arg Phe Arg
180 185 190

Ala Thr Phe Ala Ser His Val Gln Pro Gly Gln Tyr Val Leu Val Ala
195 200 205

40 Gly Val Pro Gly Leu Gln Pro Ala Arg Val Ala Ala Val Ser Thr His
210 215 220

Val Ala Leu Gly Ala Tyr Ala Pro Leu Thr Lys His Gly Thr Leu Val
45 225 230 235 240

Val Glu Asp Val Val Ala Ser Cys Phe Ala Ala Val Ala Asp His His
245 250 255

50 Leu Ala Gln Leu Ala Phe Trp Pro Leu Arg Leu Phe His Ser Leu Ala
260 265 270

Trp Gly Ser Trp Thr Pro Gly Glu Gly Val His Trp Tyr Pro Gln Leu
275 280 285

55 Leu Tyr Arg Leu Gly Arg Leu Leu Leu Glu Glu Gly Ser Phe His Pro
290 295 300

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Leu Gly Met Ser Gly Ala Gly Ser Xaa
305 310

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 64 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Gln Arg Cys Lys Asp Lys Leu Asn Ser Leu Ala Ile Ser Val Met Asn
1 5 10 15
His Trp Pro Gly Val Lys Leu Arg Val Thr Glu Gly Trp Asp Glu Asp
20 25 30
Gly His His Phe Glu Glu Ser Leu His Tyr Glu Gly Arg Ala Val Asp
35 40 45
Ile Thr Thr Ser Asp Arg Asp Lys Ser Lys Tyr Gly Thr Leu Ser Arg
50 55 60

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Gln Arg Cys Lys Glu Lys Leu Asn Ser Leu Ala Ile Ser Val Met Asn
1 5 10 15
Met Trp Pro Gly Val Lys Leu Arg Val Thr Glu Gly Trp Asp Glu Asp
20 25 30
Gly Asn His Phe Glu Asp Ser Leu His Tyr Glu Gly Arg Ala Val Asp
35 40 45
Ile Thr Thr Ser Ser Asp Arg Asp Arg Asn Lys Tyr Gly Met Phe Ala
50 55 60

Arg

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65

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Gln	Arg	Cys	Lys	Asp	Lys	Leu	Asn	Ser	Leu	Ala	Ile	Ser	Val	Met	Asn
1				5					10					15	
Leu	Trp	Pro	Gly	Val	Lys	Leu	Arg	Val	Thr	Glu	Gly	Trp	Asp	Glu	Asp
			20					25					30		
Gly	Leu	His	Ser	Glu	Glu	Ser	Leu	His	Tyr	Glu	Gly	Arg	Ala	Val	Asp
		35					40					45			
Ile	Thr	Thr	Ser	Asp	Arg	Asp	Arg	Asn	Lys	Tyr	Arg	Met	Leu	Ala	Arg
	50					55					60				

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GGAATTCCCA GCAGNTGCTA AAGGAAGCAA GNGCTNAA

38

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

TCATCGATGG ACCCAGATCG AAANCCNGCT CTC

33

5

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

10

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

20

GCTCTAGAGC TCNACNGCNA GANCGTNGC

29

(2) INFORMATION FOR SEQ ID NO:21:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: cDNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

AGCTGTCGAC GCGGCCGCTA CGTAGGTTAC CGACGTCAAG CTTAGATCTC

50

40

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

45

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

AGCTGAGATC TAAGCTTGAC GTCGGTAACC TACGTAGCGG CCGCGTCGAC

55

50

(2) INFORMATION FOR SEQ ID NO:23:

962020-60542980

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GATCGGCCAG GCAGGCCTCG CGATATCGTC ACCGCGGTAT TCGAA

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

AGTGCCAGTC GGGGCCCCCA GGGCCGCGCC

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TACCACAGCG GATGGTTCGG

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GTGGTGGTTA TGCCGATCGC

20

10 (2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TAAGAGGCCT ATAAGAGGCG G

21

25

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA

30

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AAGTCAGCCC AGAGGAGACT

20

40

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

45

(ii) MOLECULE TYPE: peptide

50

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

55

Cys Gly Pro Gly Arg Gly
1 5

(2) INFORMATION FOR SEQ ID NO:30:

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- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

AGCAGNTGCT AAAGGAAGCA AGNGCTNAA

29

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CTCNACNGCN AGANCKNGTN GCNA

24

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CTGCAGGGAT CCACCATGCG GCTTTTGACG AG

32

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CTGCAGGGAT CCTTATTCCA CACGAGGGAT T

31

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 471 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Met	Asp	Asn	His	Ser	Ser	Val	Pro	Trp	Ala	Ser	Ala	Ala	Ser	Val	Thr	1	5	10	15
Cys	Leu	Ser	Leu	Asp	Ala	Lys	Cys	His	Ser	Ser	Ser	Ser	Ser	Ser	Ser	20	25	30	
Ser	Lys	Ser	Ala	Ala	Ser	Ser	Ile	Ser	Ala	Ile	Pro	Gln	Glu	Glu	Thr	35	40	45	
Gln	Thr	Met	Arg	His	Ile	Ala	His	Thr	Gln	Arg	Cys	Leu	Ser	Arg	Leu	50	55	60	
Thr	Ser	Leu	Val	Ala	Leu	Leu	Leu	Ile	Val	Leu	Pro	Met	Val	Phe	Ser	65	70	75	80
Pro	Ala	His	Ser	Cys	Gly	Pro	Gly	Arg	Gly	Leu	Gly	Arg	His	Arg	Ala	85	90	95	
Arg	Asn	Leu	Tyr	Pro	Leu	Val	Leu	Lys	Gln	Thr	Ile	Pro	Asn	Leu	Ser	100	105	110	
Glu	Tyr	Thr	Asn	Ser	Ala	Ser	Gly	Pro	Leu	Glu	Gly	Val	Ile	Arg	Arg	115	120	125	
Asp	Ser	Pro	Lys	Phe	Lys	Asp	Leu	Val	Pro	Asn	Tyr	Asn	Arg	Asp	Ile	130	135	140	
Leu	Phe	Arg	Asp	Glu	Glu	Gly	Thr	Gly	Ala	Asp	Arg	Leu	Met	Ser	Lys	145	150	155	160
Arg	Cys	Lys	Glu	Lys	Leu	Asn	Val	Leu	Ala	Tyr	Ser	Val	Met	Asn	Glu	165	170	175	
Trp	Pro	Gly	Ile	Arg	Leu	Leu	Val	Thr	Glu	Ser	Trp	Asp	Glu	Asp	Tyr	180	185	190	

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His His Gly Gln Glu Ser Leu His Tyr Glu Gly Arg Ala Val Thr Ile
195 200 205

5 Ala Thr Ser Asp Arg Asp Gln Ser Lys Tyr Gly Met Leu Ala Arg Leu
210 215 220

Ala Val Glu Ala Gly Phe Asp Trp Val Ser Tyr Val Ser Arg Arg His
225 230 235 240

10 Ile Tyr Cys Ser Val Lys Ser Asp Ser Ser Ile Ser Ser His Val His
245 250 255

Gly Cys Phe Thr Pro Glu Ser Thr Ala Leu Leu Glu Ser Gly Val Arg
260 265 270

15 Lys Pro Leu Gly Glu Leu Ser Ile Gly Asp Arg Val Leu Ser Met Thr
275 280 285

20 Ala Asn Gly Gln Ala Val Tyr Ser Glu Val Ile Leu Phe Met Asp Arg
290 295 300

Asn Leu Glu Gln Met Gln Asn Phe Val Gln Leu His Thr Asp Gly Gly
305 310 315 320

25 Ala Val Leu Thr Val Thr Pro Ala His Leu Val Ser Val Trp Gln Pro
325 330 335

Glu Ser Gln Lys Leu Thr Phe Val Phe Ala Asp Arg Ile Glu Glu Lys
340 345 350

30 Asn Gln Val Leu Val Arg Asp Val Glu Thr Gly Glu Leu Arg Pro Gln
355 360 365

Arg Val Val Lys Val Gly Ser Val Arg Ser Lys Gly Val Val Ala Pro
370 375 380

35 Leu Thr Arg Glu Gly Thr Ile Val Val Asn Ser Val Ala Ala Ser Cys
385 390 395 400

40 Tyr Ala Val Ile Asn Ser Gln Ser Leu Ala His Trp Gly Leu Ala Pro
405 410 415

Met Arg Leu Leu Ser Thr Leu Glu Ala Trp Leu Pro Ala Lys Glu Gln
420 425 430

45 Leu His Ser Ser Pro Lys Val Val Ser Ser Ala Gln Gln Gln Asn Gly
435 440 445

50 Ile His Trp Tyr Ala Asn Ala Leu Tyr Lys Val Lys Asp Tyr Val Leu
450 455 460

Pro Gln Ser Trp Arg His Asp
465 470

55

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

08624509.0006
962040.6054.2980

(A) LENGTH: 73 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: peptide
(v) FRAGMENT TYPE: internal

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Arg Cys Lys Glu Arg Val Asn Ser Leu Ala Ile Ala Val Met His Met
1 5 10 15
Trp Pro Gly Val Arg Leu Arg Val Thr Glu Gly Trp Asp Glu Asp Gly
20 25 30
His His Leu Pro Asp Ser Leu His Tyr Glu Gly Arg Ala Leu Asp Ile
20 35 40 45
Thr Thr Ser Asp Arg Asp Arg His Lys Tyr Gly Met Leu Ala Arg Leu
50 55 60
Ala Val Glu Ala Gly Phe Asp Trp Val
65 70

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 73 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Arg Cys Lys Asp Lys Leu Asn Ala Leu Ala Ile Ser Val Met Asn Gln
1 5 10 15
Trp Pro Gly Val Lys Leu Arg Val Thr Glu Gly Trp Asp Glu Asp Gly
20 25 30
His His Ser Glu Glu Ser Leu His Tyr Glu Gly Arg Ala Val Asp Ile
35 40 45
Thr Thr Ser Asp Arg Asp Arg Ser Lys Tyr Gly Met Leu Ala Arg Leu
50 55 60
Ala Val Glu Ala Gly Phe Asp Trp Val
65 70

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(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Lys	Arg	Cys	Lys	Glu	Lys	Leu	Asn	Val	Leu	Ala	Tyr	Ser	Val	Met	Asn
1			5						10					15	
Glu	Trp	Pro	Gly	Ile	Arg	Leu	Val	Val	Thr	Glu	Ser	Trp	Asp	Glu	Asp
			20					25					30		
Tyr	His	His	Gly	Gln	Glu	Ser	Leu	His	Tyr	Glu	Gly	Arg	Ala	Val	Thr
		35					40					45			
Ile	Ala	Thr	Ser	Asp	Arg	Asp	Gln	Ser	Lys	Tyr	Gly	Met	Leu	Ala	Arg
	50					55					60				

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

AAAAGCTTTA YTGYTAYGTN GGNATHGG

28

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

AAGAATTCTA NGCRTTRTAR TTRTTNGG

28

5

(2) INFORMATION FOR SEO ID NO:40:

10

(ii) MOLECULE TYPE: peptide

15 (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEO ID NO:40:

20

Cys Gly Pro Gly Arg Gly Xaa Gly Xaa Arg Arg His Pro Lys Lys Leu
1 5 10 15

25

Thr Pro Leu Ala Tyr Lys Gln Phe Ile Pro Asn Val Ala Glu Lys Thr
20 25 30

30

Leu Gly Ala Ser Gly Arg Tyr Glu Gly Lys Ile Xaa Arg Asn Ser Glu
35 40 45

Arg Phe Lys Glu Leu Thr Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys
50 55 60

35

Asp Glu Glu Asn Thr Gly Ala Asp Arg Leu Met Thr Gln Arg Cys Lys
65 70 75 80

Asp Lys Leu Asn Xaa Leu Ala Ile Ser Val Met Asn Xaa Trp Pro Gly
85 90 95

40

Val Xaa Leu Arg Val Thr Glu Gly Trp Asp Glu Asp Gly His His Xaa
100 105 110

Glu Glu Ser Leu His Tyr Glu Gly Arg Ala Val Asp Ile Thr Thr Ser
115 120 125

45

Asp Arg Asp Xaa Ser Lys Tyr Gly Xaa Leu Xaa Arg Leu Ala Val Glu
130 135 140

50

Ala Gly Phe Asp Trp Val Tyr Tyr Glu Ser Lys Ala His Ile His Cys
145 150 155 160

Ser Val Lys Ala Glu Asn Ser Val Ala Ala Lys Ser Gly Gly Cys Phe
165 170 175

55

Pro Gly Ser Ala Xaa Val Xaa Leu Xaa Xaa Gly Gly Xaa Lys Xaa Val
180 185 190

Lys Asp Leu Xaa Pro Gly Asp Xaa Val Leu Ala Ala Asp Xaa Xaa Gly
195 200 205

Xaa Leu Xaa Xaa Ser Asp Phe Xaa Xaa Phe Xaa Asp Arg
210 215 220

5

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 167 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Cys Gly Pro Gly Arg Gly Xaa Xaa Xaa Arg Arg Xaa Xaa Xaa Pro Lys
1 5 10 15
Xaa Leu Xaa Pro Leu Xaa Tyr Lys Gln Phe Xaa Pro Xaa Xaa Xaa Glu
20 25 30
Xaa Thr Leu Gly Ala Ser Gly Xaa Xaa Glu Gly Xaa Xaa Xaa Arg Xaa
35 40 45
Ser Glu Arg Phe Xaa Xaa Leu Thr Pro Asn Tyr Asn Pro Asp Ile Ile
50 55 60
Phe Lys Asp Glu Glu Asn Xaa Gly Ala Asp Arg Leu Met Thr Xaa Arg
65 70 75 80
Cys Lys Xaa Xaa Xaa Asn Xaa Leu Ala Ile Ser Val Met Asn Xaa Trp
85 90 95
Pro Gly Val Xaa Leu Arg Val Thr Glu Gly Xaa Asp Glu Asp Gly His
100 105 110
His Xaa Xaa Xaa Ser Leu His Tyr Glu Gly Arg Ala Xaa Asp Ile Thr
115 120 125
Thr Ser Asp Arg Asp Xaa Xaa Lys Tyr Gly Xaa Leu Xaa Arg Leu Ala
130 135 140
Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr Glu Ser Xaa Xaa His Xaa
145 150 155 160
His Xaa Ser Val Lys Xaa Xaa
165

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 4344 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..4341

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

20	ATG GCC TCG GCT GGT AAC GCC GCC GAG CCC CAG GAC CGC GGC GGC GGC	48
	Met Ala Ser Ala Gly Asn Ala Ala Glu Pro Gln Asp Arg Gly Gly Gly	
	1 5 10 15	
25	GGC AGC GGC TGT ATC GGT GCC CCG GGA CGG CCG GCT GGA GGC GGG AGG	96
	Gly Ser Gly Cys Ile Gly Ala Pro Gly Arg Pro Ala Gly Gly Gly Arg	
	20 25 30	
30	CGC AGA CGG ACG GGG GGG CTG CGC CGT GCT GCC GCG CCG GAC CGG GAC	144
	Arg Arg Arg Thr Gly Gly Leu Arg Arg Ala Ala Ala Pro Asp Arg Asp	
	35 40 45	
35	TAT CTG CAC CGG CCC AGC TAC TGC GAC GCC GCC TTC GCT CTG GAG CAG	192
	Tyr Leu His Arg Pro Ser Tyr Cys Asp Ala Ala Phe Ala Leu Glu Gln	
	50 55 60	
40	ATT TCC AAG GGG AAG GCT ACT GGC CGG AAA GCG CCA CTG TGG CTG AGA	240
	Ile Ser Lys Gly Lys Ala Thr Gly Arg Lys Ala Pro Leu Trp Leu Arg	
	65 70 75 80	
45	GCG AAG TTT CAG AGA CTC TTA TTT AAA CTG GGT TGT TAC ATT CAA AAA	288
	Ala Lys Phe Gln Arg Leu Leu Phe Lys Leu Gly Cys Tyr Ile Gln Lys	
	85 90 95	
50	AAC TGC GGC AAG TTC TTG GTT GTG GGC CTC CTC ATA TTT GGG GCC TTC	336
	Asn Cys Gly Lys Phe Leu Val Val Gly Leu Leu Ile Phe Gly Ala Phe	
	100 105 110	
55	GCG GTG GGA TTA AAA GCA GCG AAC CTC GAG ACC AAC GTG GAG GAG CTG	384
	Ala Val Gly Leu Lys Ala Ala Asn Leu Glu Thr Asn Val Glu Glu Leu	
	115 120 125	
60	TGG GTG GAA GTT GGA GGA CGA GTA AGT CGT GAA TTA AAT TAT ACT CGC	432
	Trp Val Glu Val Gly Gly Arg Val Ser Arg Glu Leu Asn Tyr Thr Arg	
	130 135 140	
65	CAG AAG ATT GGA GAA GAG GCT ATG TTT AAT CCT CAA CTC ATG ATA CAG	480
	Gln Lys Ile Gly Glu Glu Ala Met Phe Asn Pro Gln Leu Met Ile Gln	
	145 150 155 160	
70	ACC CCT AAA GAA GAA GGT GCT AAT GTC CTG ACC ACA GAA GCG CTC CTA	528
	Thr Pro Lys Glu Glu Gly Ala Asn Val Leu Thr Thr Glu Ala Leu Leu	

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	165	170	175	
5	CAA CAC CTG GAC TCG GCA CTC CAG GCC AGC CGT GTC CAT GTA TAC ATG Gln His Leu Asp Ser Ala Leu Gln Ala Ser Arg Val His Val Tyr Met 180 185 190	576		
10	TAC AAC AGG CAG TGG AAA TTG GAA CAT TTG TGT TAC AAA TCA GGA GAG Tyr Asn Arg Gln Trp Lys Leu Glu His Leu Cys Tyr Lys Ser Gly Glu 195 200 205	624		
15	CTT ATC ACA GAA ACA GGT TAC ATG GAT CAG ATA ATA GAA TAT CTT TAC Leu Ile Thr Glu Thr Gly Tyr Met Asp Gln Ile Ile Glu Tyr Leu Tyr 210 215 220	672		
20	CCT TGT TTG ATT ATT ACA CCT TTG GAC TGC TTC TGG GAA GGG GCG AAA Pro Cys Leu Ile Ile Thr Pro Leu Asp Cys Phe Trp Glu Gly Ala Lys 225 230 235 240	720		
25	TTA CAG TCT GGG ACA GCA TAC CTC CTA GGT AAA CCT CCT TTG CGG TGG Leu Gln Ser Gly Thr Ala Tyr Leu Leu Gly Lys Pro Pro Leu Arg Trp 245 250 255	768		
30	ACA AAC TTC GAC CCT TTG GAA TTC CTG GAA GAG TTA AAG AAA ATA AAC Thr Asn Phe Asp Pro Leu Glu Phe Leu Glu Glu Leu Lys Lys Ile Asn 260 265 270	816		
35	TAT CAA GTG GAC AGC TGG GAG GAA ATG CTG AAT AAG GCT GAG GTT GGT Tyr Gln Val Asp Ser Trp Glu Glu Met Leu Asn Lys Ala Glu Val Gly 275 280 285	864		
40	CAT GGT TAC ATG GAC CGC CCC TGC CTC AAT CCG GCC GAT CCA GAC TGC His Gly Tyr Met Asp Arg Pro Cys Leu Asn Pro Ala Asp Pro Asp Cys 290 295 300	912		
45	CCC GCC ACA GCC CCC AAC AAA AAT TCA ACC AAA CCT CTT GAT ATG GCC Pro Ala Thr Ala Pro Asn Lys Asn Ser Thr Lys Pro Leu Asp Met Ala 305 310 315 320	960		
50	CTT GTT TTG AAT GGT GGA TGT CAT GGC TTA TCC AGA AAG TAT ATG CAC Leu Val Leu Asn Gly Gly Cys His Gly Leu Ser Arg Lys Tyr Met His 325 330 335	1008		
55	TGG CAG GAG GAG TTG ATT GTG GGT GGC ACA GTC AAG AAC AGC ACT GGA Trp Gln Glu Glu Leu Ile Val Gly Gly Thr Val Lys Asn Ser Thr Gly 340 345 350	1056		
60	AAA CTC GTC AGC GCC CAT GCC CTG CAG ACC ATG TTC CAG TTA ATG ACT Lys Leu Val Ser Ala His Ala Leu Gln Thr Met Phe Gln Leu Met Thr 355 360 365	1104		
65	CCC AAG CAA ATG TAC GAG CAC TTC AAG GGG TAC GAG TAT GTC TCA CAC Pro Lys Gln Met Tyr Glu His Phe Lys Gly Tyr Glu Tyr Val Ser His 370 375 380	1152		
70	ATC AAC TGG AAC GAG GAC AAA GCG GCA GCC ATC CTG GAG GCC TGG CAG Ile Asn Trp Asn Glu Asp Lys Ala Ala Ala Ile Leu Glu Ala Trp Gln 385 390 395 400	1200		

	AGG	ACA	TAT	GTG	GAG	GTG	GTT	CAT	CAG	AGT	GTC	GCA	CAG	AAC	TCC	ACT	1248
	Arg	Thr	Tyr	Val	Glu	Val	Val	His	Gln	Ser	Val	Ala	Gln	Asn	Ser	Thr	
				405					410						415		
5	CAA	AAG	GTG	CTT	TCC	TTC	ACC	ACC	ACG	ACC	CTG	GAC	GAC	ATC	CTG	AAA	1296
	Gln	Lys	Val	Leu	Ser	Phe	Thr	Thr	Thr	Thr	Leu	Asp	Asp	Ile	Leu	Lys	
				420					425					430			
10	TCC	TTC	TCT	GAC	GTC	AGT	GTC	ATC	CGC	GTG	GCC	AGC	GGC	TAC	TTA	CTC	1344
	Ser	Phe	Ser	Asp	Val	Ser	Val	Ile	Arg	Val	Ala	Ser	Gly	Tyr	Leu	Leu	
				435				440					445				
15	ATG	CTC	GCC	TAT	GCC	TGT	CTA	ACC	ATG	CTG	CGC	TGG	GAC	TGC	TCC	AAG	1392
	Met	Leu	Ala	Tyr	Ala	Cys	Leu	Thr	Met	Leu	Arg	Trp	Asp	Cys	Ser	Lys	
		450					455					460					
20	TCC	CAG	GGT	GCC	GTG	GGG	CTG	GCT	GGC	GTC	CTG	CTG	GTT	GCA	CTG	TCA	1440
	Ser	Gln	Gly	Ala	Val	Gly	Leu	Ala	Gly	Val	Leu	Leu	Val	Ala	Leu	Ser	
	465					470					475					480	
25	GTG	GCT	GCA	GGA	CTG	GGC	CTG	TGC	TCA	TTG	ATC	GGA	ATT	TCC	TTT	AAC	1488
	Val	Ala	Ala	Gly	Leu	Gly	Leu	Cys	Ser	Leu	Ile	Gly	Ile	Ser	Phe	Asn	
				485						490					495		
30	GCT	GCA	ACA	ACT	CAG	GTT	TTG	CCA	TTT	CTC	GCT	CTT	GGT	GTT	GGT	GTG	1536
	Ala	Ala	Thr	Thr	Gln	Val	Leu	Pro	Phe	Leu	Ala	Leu	Gly	Val	Gly	Val	
				500					505					510			
35	GAT	GAT	GTT	TTT	CTT	CTG	GCC	CAC	GCC	TTC	AGT	GAA	ACA	GGA	CAG	AAT	1584
	Asp	Asp	Val	Phe	Leu	Leu	Ala	His	Ala	Phe	Ser	Glu	Thr	Gly	Gln	Asn	
			515					520					525				
40	AAA	AGA	ATC	CCT	TTT	GAG	GAC	AGG	ACC	GGG	GAG	TGC	CTG	AAG	CGC	ACA	1632
	Lys	Arg	Ile	Pro	Phe	Glu	Asp	Arg	Thr	Gly	Glu	Cys	Leu	Lys	Arg	Thr	
		530					535					540					
45	GGA	GCC	AGC	GTG	GCC	CTC	ACG	TCC	ATC	AGC	AAT	GTC	ACA	GCC	TTC	TTC	1680
	Gly	Ala	Ser	Val	Ala	Leu	Thr	Ser	Ile	Ser	Asn	Val	Thr	Ala	Phe	Phe	
	545					550					555					560	
50	ATG	GCC	GCG	TTA	ATC	CCA	ATT	CCC	GCT	CTG	CGG	GCG	TTC	TCC	CTC	CAG	1728
	Met	Ala	Ala	Leu	Ile	Pro	Ile	Pro	Ala	Leu	Arg	Ala	Phe	Ser	Leu	Gln	
				565					570						575		
55	GCA	GCG	GTA	GTA	GTG	GTG	TTC	AAT	TTT	GCC	ATG	GTT	CTG	CTC	ATT	TTT	1776
	Ala	Ala	Val	Val	Val	Val	Phe	Asn	Phe	Ala	Met	Val	Leu	Leu	Ile	Phe	
				580					585					590			
60	CCT	GCA	ATT	CTC	AGC	ATG	GAT	TTA	TAT	CGA	CGC	GAG	GAC	AGG	AGA	CTG	1824
	Pro	Ala	Ile	Leu	Ser	Met	Asp	Leu	Tyr	Arg	Arg	Glu	Asp	Arg	Arg	Leu	
			595					600					605				
65	GAT	ATT	TTC	TGC	TGT	TTT	ACA	AGC	CCC	TGC	GTC	AGC	AGA	GTG	ATT	CAG	1872
	Asp	Ile	Phe	Cys	Cys	Phe	Thr	Ser	Pro	Cys	Val	Ser	Arg	Val	Ile	Gln	
		610					615					620					
70	GTT	GAA	CCT	CAG	GCC	TAC	ACC	GAC	ACA	CAC	GAC	AAT	ACC	CGC	TAC	AGC	1920
	Val	Glu	Pro	Gln	Ala	Tyr	Thr	Asp	Thr	His	Asp	Asn	Thr	Arg	Tyr	Ser	

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	625		630		635		640	
5	CCC CCA CCT CCC TAC AGC AGC CAC AGC TTT GCC CAT GAA ACG CAG ATT Pro Pro Pro Pro Tyr Ser Ser His Ser Phe Ala His Glu Thr Gln Ile		645		650		655	1968
10	ACC ATG CAG TCC ACT GTC CAG CTC CGC ACG GAG TAC GAC CCC CAC ACG Thr Met Gln Ser Thr Val Gln Leu Arg Thr Glu Tyr Asp Pro His Thr		660		665		670	2016
15	CAC GTG TAC TAC ACC ACC GCT GAG CCG CGC TCC GAG ATC TCT GTG CAG His Val Tyr Thr Thr Ala Glu Pro Arg Ser Glu Ile Ser Val Gln		675		680		685	2064
20	CCC GTC ACC GTG ACA CAG GAC ACC CTC AGC TGC CAG AGC CCA GAG AGC Pro Val Thr Val Thr Gln Asp Thr Leu Ser Cys Gln Ser Pro Glu Ser		690		695		700	2112
25	ACC AGC TCC ACA AGG GAC CTG CTC TCC CAG TTC TCC GAC TCC AGC CTC Thr Ser Ser Thr Arg Asp Leu Leu Ser Gln Phe Ser Asp Ser Ser Leu		705		710		715	2160
30	CAC TGC CTC GAG CCC CCC TGT ACG AAG TGG ACA CTC TCA TCT TTT GCT His Cys Leu Glu Pro Pro Cys Thr Lys Trp Thr Leu Ser Ser Phe Ala		725		730		735	2208
35	GAG AAG CAC TAT GCT CCT TTC CTC TTG AAA CCA AAA GCC AAG GTA GTG Glu Lys His Tyr Ala Pro Phe Leu Leu Lys Pro Lys Ala Lys Val Val		740		745		750	2256
40	GTG ATC TTC CTT TTT CTG GGC TTG CTG GGG GTC AGC CTT TAT GGC ACC Val Ile Phe Leu Phe Leu Gly Leu Leu Gly Val Ser Leu Tyr Gly Thr		755		760		765	2304
45	ACC CGA GTG AGA GAC GGG CTG GAC CTT ACG GAC ATT GTA CCT CGG GAA Thr Arg Val Arg Asp Gly Leu Asp Leu Thr Asp Ile Val Pro Arg Glu		770		775		780	2352
50	ACC AGA GAA TAT GAC TTT ATT GCT GCA CAA TTC AAA TAC TTT TCT TTC Thr Arg Glu Tyr Asp Phe Ile Ala Ala Gln Phe Lys Tyr Phe Ser Phe		785		790		795	2400
55	TAC AAC ATG TAT ATA GTC ACC CAG AAA GCA GAC TAC CCG AAT ATC CAG Tyr Asn Met Tyr Ile Val Thr Gln Lys Ala Asp Tyr Pro Asn Ile Gln		805		810		815	2448
60	CAC TTA CTT TAC GAC CTA CAC AGG AGT TTC AGT AAC GTG AAG TAT GTC His Leu Leu Tyr Asp Leu His Arg Ser Phe Ser Asn Val Lys Tyr Val		820		825		830	2496
65	ATG TTG GAA GAA AAC AAA CAG CTT CCC AAA ATG TGG CTG CAC TAC TTC Met Leu Glu Glu Asn Lys Gln Leu Pro Lys Met Trp Leu His Tyr Phe		835		840		845	2544
70	AGA GAC TGG CTT CAG GGA CTT CAG GAT GCA TTT GAC AGT GAC TGG GAA Arg Asp Trp Leu Gln Gly Leu Gln Asp Ala Phe Asp Ser Asp Trp Glu		850		855		860	2592

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	ACC GGG AAA ATC ATG CCA AAC AAT TAC AAG AAT GGA TCA GAC GAT GGA	2640
	Thr Gly Lys Ile Met Pro Asn Asn Tyr Lys Asn Gly Ser Asp Asp Gly	
	865 870 875 880	
5	GTC CTT GCC TAC AAA CTC CTG GTG CAA ACC GGC AGC CGC GAT AAG CCC	2688
	Val Leu Ala Tyr Lys Leu Leu Val Gln Thr Gly Ser Arg Asp Lys Pro	
	885 890 895	
10	ATC GAC ATC AGC CAG TTG ACT AAA CAG CGT CTG GTG GAT GCA GAT GGC	2736
	Ile Asp Ile Ser Gln Leu Thr Lys Gln Arg Leu Val Asp Ala Asp Gly	
	900 905 910	
15	ATC ATT AAT CCC AGC GCT TTC TAC ATC TAC CTG ACG GCT TGG GTC AGC	2784
	Ile Ile Asn Pro Ser Ala Phe Tyr Ile Tyr Leu Thr Ala Trp Val Ser	
	915 920 925	
20	AAC GAC CCC GTC GCG TAT GCT GCC TCC CAG GCC AAC ATC CGG CCA CAC	2832
	Asn Asp Pro Val Ala Tyr Ala Ala Ser Gln Ala Asn Ile Arg Pro His	
	930 935 940	
25	CGA CCA GAA TGG GTC CAC GAC AAA GCC GAC TAC ATG CCT GAA ACA AGG	2880
	Arg Pro Glu Trp Val His Asp Lys Ala Asp Tyr Met Pro Glu Thr Arg	
	945 950 955 960	
30	CTG AGA ATC CCG GCA GCA GAG CCC ATC GAG TAT GCC CAG TTC CCT TTC	2928
	Leu Arg Ile Pro Ala Ala Glu Pro Ile Glu Tyr Ala Gln Phe Pro Phe	
	965 970 975	
35	TAC CTC AAC GGG TTG CGG GAC ACC TCA GAC TTT GTG GAG GCA ATT GAA	2976
	Tyr Leu Asn Gly Leu Arg Asp Thr Ser Asp Phe Val Glu Ala Ile Glu	
	980 985 990	
40	AAA GTA AGG ACC ATC TGC AGC AAC TAT ACG AGC CTG GGG CTG TCC AGT	3024
	Lys Val Arg Thr Ile Cys Ser Asn Tyr Thr Ser Leu Gly Leu Ser Ser	
	995 1000 1005	
45	TAC CCC AAC GGC TAC CCC TTC CTC TTC TGG GAG CAG TAC ATC GGC CTC	3072
	Tyr Pro Asn Gly Tyr Pro Phe Leu Phe Trp Glu Gln Tyr Ile Gly Leu	
	1010 1015 1020	
50	CGC CAC TGG CTG CTG CTG TTC ATC AGC GTG GTG TTG GCC TGC ACA TTC	3120
	Arg His Trp Leu Leu Phe Ile Ser Val Val Leu Ala Cys Thr Phe	
	1025 1030 1035 1040	
55	CTC GTG TGC GCT GTC TTC CTT CTG AAC CCC TGG ACG GCC GGG ATC ATT	3168
	Leu Val Cys Ala Val Phe Leu Leu Asn Pro Trp Thr Ala Gly Ile Ile	
	1045 1050 1055	
60	GTG ATG GTC CTG GCG CTG ATG ACG GTC GAG CTG TTC GGC ATG ATG GGC	3216
	Val Met Val Leu Ala Leu Met Thr Val Glu Leu Phe Gly Met Met Gly	
	1060 1065 1070	
65	CTC ATC GGA ATC AAG CTC AGT GCC GTG CCC GTG GTC ATC CTG ATC GCT	3264
	Leu Ile Gly Ile Lys Leu Ser Ala Val Pro Val Val Ile Leu Ile Ala	
	1075 1080 1085	
70	TCT GTT GGC ATA GGA GTG GAG TTC ACC GTT CAC GTT GCT TTG GCC TTT	3312
	Ser Val Gly Ile Gly Val Glu Phe Thr Val His Val Ala Leu Ala Phe	

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	1090	1095	1100	
5	CTG ACG GCC ATC GGC GAC AAG AAC CGC AGG GCT GTG CTT GCC CTG GAG Leu Thr Ala Ile Gly Asp Lys Asn Arg Arg Ala Val Leu Ala Leu Glu 1105 1110 1115 1120			3360
10	CAC ATG TTT GCA CCC GTC CTG GAT GGC GCC GTG TCC ACT CTG CTG GGA His Met Phe Ala Pro Val Leu Asp Gly Ala Val Ser Thr Leu Leu Gly 1125 1130 1135			3408
15	GTG CTG ATG CTG GCG GGA TCT GAG TTC GAC TTC ATT GTC AGG TAT TTC Val Leu Met Leu Ala Gly Ser Glu Phe Asp Phe Ile Val Arg Tyr Phe 1140 1145 1150			3456
20	TTT GCT GTG CTG GCG ATC CTC ACC ATC CTC GGC GTT CTC AAT GGG CTG Phe Ala Val Leu Ala Ile Leu Thr Ile Leu Gly Val Leu Asn Gly Leu 1155 1160 1165			3504
25	GTT TTG CTT CCC GTG CTT TTG TCT TTC TTT GGA CCA TAT CCT GAG GTG Val Leu Leu Pro Val Leu Leu Ser Phe Phe Gly Pro Tyr Pro Glu Val 1170 1175 1180			3552
30	TCT CCA GCC AAC GGC TTG AAC CGC CTG CCC ACA CCC TCC CCT GAG CCA Ser Pro Ala Asn Gly Leu Asn Arg Leu Pro Thr Pro Ser Pro Glu Pro 1185 1190 1195 1200			3600
35	CCC CCC AGC GTG GTC CGC TTC GCC ATG CCG CCC GGC CAC ACG CAC AGC Pro Pro Ser Val Val Arg Phe Ala Met Pro Pro Gly His Thr His Ser 1205 1210 1215			3648
40	GGG TCT GAT TCC TCC GAC TCG GAG TAT AGT TCC CAG ACG ACA GTG TCA Gly Ser Asp Ser Ser Asp Ser Glu Tyr Ser Ser Gln Thr Thr Val Ser 1220 1225 1230			3696
45	GGC CTC AGC GAG GAG CTT CGG CAC TAC GAG GCC CAG CAG GGC GCG GGA Gly Leu Ser Glu Glu Leu Arg His Tyr Glu Ala Gln Gln Gly Ala Gly 1235 1240 1245			3744
50	GGC CCT GCC CAC CAA GTG ATC GTG GAA GCC ACA GAA AAC CCC GTC TTC Gly Pro Ala His Gln Val Ile Val Glu Ala Thr Glu Asn Pro Val Phe 1250 1255 1260			3792
55	GCC CAC TCC ACT GTG GTC CAT CCC GAA TCC AGG CAT CAC CCA CCC TCG Ala His Ser Thr Val Val His Pro Glu Ser Arg His His Pro Pro Ser 1265 1270 1275 1280			3840
60	AAC CCG AGA CAG CAG CCC CAC CTG GAC TCA GGG TCC CTG CCT CCC GGA Asn Pro Arg Gln Gln Pro His Leu Asp Ser Gly Ser Leu Pro Pro Gly 1285 1290 1295			3888
65	CGG CAA GGC CAG CAG CCC CGC AGG GAC CCC CCC AGA GAA GGC TTG TGG Arg Gln Gly Gln Gln Pro Arg Arg Asp Pro Pro Arg Glu Gly Leu Trp 1300 1305 1310			3936
70	CCA CCC CTC TAC AGA CCG CGC AGA GAC GCT TTT GAA ATT TCT ACT GAA Pro Pro Leu Tyr Arg Pro Arg Arg Asp Ala Phe Glu Ile Ser Thr Glu 1315 1320 1325			3984

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GGG CAT TCT GGC CCT AGC AAT AGG GCC CGC TGG GGC CCT CGC GGG GCC 4032
Gly His Ser Gly Pro Ser Asn Arg Ala Arg Trp Gly Pro Arg Gly Ala
1330 1335 1340

5 CGT TCT CAC AAC CCT CGG AAC CCA GCG TCC ACT GCC ATG GGC AGC TCC 4080
Arg Ser His Asn Pro Arg Asn Pro Ala Ser Thr Ala Met Gly Ser Ser
1345 1350 1355 1360

10 GTG CCC GGC TAC TGC CAG CCC ATC ACC ACT GTG ACG GCT TCT GCC TCC 4128
Val Pro Gly Tyr Cys Gln Pro Ile Thr Thr Val Thr Ala Ser Ala Ser
1365 1370 1375

15 GTG ACT GTC GCC GTG CAC CCG CCG CCT GTC CCT GGG CCT GGG CGG AAC 4176
Val Thr Val Ala Val His Pro Pro Val Pro Gly Pro Gly Arg Asn
1380 1385 1390

20 CCC CGA GGG GGA CTC TGC CCA GGC TAC CCT GAG ACT GAC CAC GGC CTG 4224
Pro Arg Gly Gly Leu Cys Pro Gly Tyr Pro Glu Thr Asp His Gly Leu
1395 1400 1405

25 TTT GAG GAC CCC CAC GTG CCT TTC CAC GTC CGG TGT GAG AGG AGG GAT 4272
Phe Glu Asp Pro His Val Pro Phe His Val Arg Cys Glu Arg Arg Asp
1410 1415 1420

30 TCG AAG GTG GAA GTC ATT GAG CTG CAG GAC GTG GAA TGC GAG GAG AGG 4320
Ser Lys Val Glu Val Ile Glu Leu Gln Asp Val Glu Cys Glu Glu Arg
1425 1430 1435 1440

35 CCC CGG GGA AGC AGC TCC AAC TGA 4344
Pro Arg Gly Ser Ser Ser Asn
1445

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

ACCGAGGGCT GGGACGAAGA TGGC 24

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

962020-6054980

(ii) MOLECULE TYPE: cDNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

CGCTCGGTCG TACGGCATGA ACGAC

25

10 (2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs

(B) TYPE: nucleic acid

15 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

ATGGGGATGT GTGTGTGGTC AAGTGTA

27

25

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

30 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

40 TTCACAGACT CTCAAAGTGT ATTTT

25

(2) INFORMATION FOR SEQ ID NO:47:

45 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Met Gly Ser Ser His His His His His Leu Val Pro Arg Gly Ser

1

5

10

15

His Met

08674509.070296